## STIC-Biotech/ChemLib

From: Sent:

Ibrahim, Medina A.

Thursday, June 05, 2003 5:39 PM STIC-Biotech/ChemLib

T : Subject:

10/090, 035

(ST.C)

Please search the following:

DNA encoding SEQ ID NO:2 or 4.
 SEQ ID NO:1-4.
 oligo of SEQ ID NO:1 and 3

Please search both commercial and patent databases, including pending. Thanks

Medina A. Ibrahim Patent Examiner GAU:1638 CM1-9E03 mailbox-9E12 (703)306-5822

> **Edward Hart** Technicai Info. Specialist STIC/Biotech CMI 6B02 Tel: 305-9203

Searcher:
Phone:
Location:
Date Picked Up: 6 6/03
Date Completed: 6/16/33 Searcher Prep/Review:
Searcher Prep/Review:
Clerical:
Online time:

TYPE OF SEARCH:/	
NA Sequences:	
AA Sequences:	-
Structures:	
Bibliographic:	
Litigation:	
Full text:	
Patent Family:	
Other:	

(where applic.)

Lexis/Nexis: Sequence Sys.: (() WWW/Internet: Other (specify):

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•

Pending Nucleic Acid and/or Pending Amino Acid database searches now generate two sets of results. These databases were split into to two parts to reduce the time needed to update the databases daily. The split freed up more machine time for processing searches.

Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions, .rnpm and .rnpn

Searches run against the Amino Acid Pending database produce two sets of results, with the extensions, .rapm and .rapn

The Pending database search results should not be left in the case because they contain data that is confidential.

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## STIC SEARCH RESULTS

## Biotech-Chem Library

Questions about the scope or the results of the search? Contact the searcher or contact:

Mary Hale, Information Branch Supervisor 308-4258, CM1-1E01

oluntary Results Feedback Form	
> I am an examiner in Workgroup: Example: 1610	_
Relevant prior art found, search results used as follows:	
☐ 102 rejection	
103 rejection	
Cited as being of interest.	
Helped examiner better understand the invention.	
Helped examiner better understand the state of the art in their technology.	
Types of relevant prior art found:	
☐ Foreign Patent(s)	
<ul> <li>Non-Patent Literature         <ul> <li>(journal articles, conference proceedings, new product announcements etc.)</li> </ul> </li> </ul>	
Relevant prior art <b>not found:</b>	
Results verified the lack of relevant prior art (helped determine patentability).	
Results were not useful in determining patentability or understanding the invention.	
omments:	

Drop off or send completed forms to STIC/Biotech-Chem:Library, GM1⊫Circ-Desk



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M74590 Mouse delta
M73963 Mus musculu
L13969 Mouse delta
AP005381 Oryza sat
AP005485 Oryza sat
AP005485 Oryza sat
AP005960 Mus muscu
AE0659 Raltus no
AL646059 Ralstonia
AL16130 Mus muscu
AL646081 Ralstonia
AL16130 Mus muscu
Continuation (3 of
AP110745 Mus muscu
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AP110748 Homo sapi
AP000853 Homo sapi
AP0010853 Homo sapi
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AC091071 Oryza sat
AP0003436 Oryza sat
AC09108 Oryza sat
AJ22802 Sporobolu
AF291784 Sinorhizo
AF003103 Arabidops
AF002598 Arabidops
AF003563 Arabidops
AE004561 Pasudomon
ALIGIS90 Arabidops
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AB023233 Homo sap1
AL333821 Neurospor
AC067762 Homo sap1
AL138704 Human DNA
AC091884 Homo sap1
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                                                                                        June 16, 2003, 08:47:15; Search time 1860 Seconds (without alignments) 1455.140 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                              4109280
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Direct Submission

AL Direct Submission

AL Direct Submission

AL Direct Submission

AL Submitted (14-Mar-2001) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan

2-1-2, Tsukuba, Lbaraki 305-8602, Japan

(B-mail:tsasakimias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7468)

On May 15, 2002 this sequence version replaced gi:18181981.

On May 15, 2002 this sequence version replaced gi:18181981.

On May 15, 2002 this sequence version replaced gi:18181981.

On May 15, 2002 this sequence version replaced gi:18181981.

On May 15, 2002 this sequence version replaced gi:18181981.

On May 15, 2002 this sequence version replaced gi:18181981.

On May 15, 2002 this sequence version replaced gi:18181981.

On May 15, 2002 this sequence version replaced gi:18181981.

On May 15, 2002 this sequence version as searched against (ctp://nobi.nlm.nlm.gn/pas/Ab) and the cDNA sequence database at (ftp://nobi.nlm.nlm.gn/pas/Ab) and the cDNA sequence database at (ftp://nobi.nlm.nlm.gn/pas/Ab) and the cDNA sequence database at (ftp://nobi.nlm.nlm.gn/pas/Ab) and the cDNA sequence database at the interieve on a database with BLASTW 2.0 with the corresponding DDBJ accession no. and RGP clone ID.

A gene with identity or significant homology to aprotein is classified based on the protein name to indicate the homology to any protein but with EST homology (covering significant homology to any protein but with EST homology (covering significant homology to any protein but with EST homology (covering significant homology to any protein and protein in a gene predicted with a genemone of P04456E05 clone has an overlap with P0470Al12 (DDBJ: Ap003436) at the position 130,058 to 173,699 of 3' end Detailed annotation of this entry is available at nuclearing of this entry is available at http://rgp.dna.affrc.go.jp/Genomeseq.html.
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                                                                                                                                                                                                                                                                                          Embryophyta; Tracheophyta;
                      Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, PAC clone:P0456E05.
                                                                                                                                                                               Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA,
clone:P0456E05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Oryza sativa (japonica cultivar-group)"
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Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                                                                                                                                                                                                                                       Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                  VERSION
KEYWORDS
SOURCE
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COMMENT

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DGTLNKLSHLARRYDDFTDYTNHMLDDKQNQLLQMGVMLSTATVVITAGVAVVGLFGM
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37701.37823.3801
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similar to Arabidopsis thaliana chromosome 3, At3948360
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/db_xref="G1:20804925"
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/gene="P0456E05.3"
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ACO91071.1 GI:13450004
HTG: HTG2_PHASE2.
Oryza sativa (japonica cultivar-group).
Spermatophyta: astiva (japonica cultivar-group).
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Ehrhartoideae: Oryzaa.
I (bases 1 to 174218)
S Lee, J. -S., Hahn, J. -H., Yoon, U. -H., Lee, M. -C., Yun, D. -W., Kim, H. -I.
Oryza sativa PAC P0456E05 genomic sequence
                                                                                                           60 GlyhisglyPheValValargGluThrargValGluGluAspileAsnThrGysThrGly 79
157400 AACGACTACCTGATGGTGCGCGAGACCAAGGTGGAGGAGGACTTCAACACCTGCACGGC 157341
                                    Upsess 1 to 174218)
Hahn,J.-H., Eun,M.Y. and Kim,H.-I.
Hahn,J.-H., Eun,M.Y. and Kim,H.-I.
Direct Submission
Submitted (127-MAR-2001) Rice Genome Sequencing Project, National
Institute of Agricultural Science and Technology(NIAST), RDA, 249
Seodun-dong, Suwon 441-707, Korea (E-mail:jhhahn@rda.go.kr,
Tel:82-31-290-0309, Fax:82-31-290-0308)
The PAC clone was provided by Japanese Rice Genome Research Program
                                                                                                                                                                                                                                                                                                                                                                                                      AC091071 174218 bp DNA linear HTG 27-MAR-2001 Oryza sativa (japonica cultivar-group) chromosome 1 clone P0456E05, *** SEQUENCING IN PROGRESS ***, 3 ordered pieces.
                  29
40 GluValAspThrValSerArgAlaGlyAlaAsnHisHisHisHisHisGlyHisHisGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Oryza sativa (japonica cultivar-group)"
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1 53113: contig of 53113 bp in length 53114 53213: gap of unknown length 17404: contig of 119191 bp in length 17404: contig of insurance of 17428 172504: gap of unknown length 172505 174218: contig of 1714 bp in length.
                                                                                                                                                                                                                                                               202 others
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57
14
19
4
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Mismatches:
Indels:
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38377 c 37185 g 49417 t
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JOURNAL
REFERENCE
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AUTHORS
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KEYWORDS
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JOURNAL
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AC091071
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/db_xref="G1:080430"
/translation="WAASRRLARKLPSLISKHQRLISPEIDVEQAAESPASSSSIPLD
PSLPIAPLAVSHLEPREPLALESWHASTPAALLRILRRAHHPRIAALDIHLLIAAA
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RKAILARAASGDIFAASDALASLRRAADSPLPAEFVIILHALARRRHEDTVRFYGE
WTGTHRVHPDVYTFVIILISSCRAGVDAAMRWFOEMRRNSCSPTGVSFNILMRGFFR
EGRCKEGIKVARBULQLGFGLSVASMEIMINGLCRGGEPLKAAEVFIEFLVDGVVPEG
MMGRWVAAEIVPDTISCNYIFEALCEAGRFVDANRLEAGAEVEIEFLDVGGVPEG
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complement(join(54710. .55150,55176. .55310,55441. .55668))
/gene="P0456E05.9"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complement(join(40277. .40417,40717. .40773,40875. .41073,4173. .41300,41399. .41504,41677. .41756,42145. .42242,42324. .42437,42523. .42663,42757. .42841,43717. .44055))
                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="P0456E05.7" 44055/
/foote="contains ESTs AU101665(R2414),D24709(R2594)
similar to Arabidopsis thaliana chromosome 5, At5g14420
unknown protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="hypothetical protein
similar to salt-inducible protein"
/codon_start=1
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Matches:
Conservative:
Mismatches:
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/db_xref="G1:20804929"
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/gene="P0456E05.8"
51367. .52887
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1205,11289, 10841,11094, .11205,11289, .11432,11817, .11921, 12916, .12129,12315, .12430,12535, .12636,12715, .12828, .12916, .12972,13312, .1388,13356, .13409,13798, .13872, /gene="popt,70,1389", .14480)
                                                                                                                                                                                                                                                                                                                                                                          join(10813. ..10841,11094. .11205,11289. .11432,11817. .11921,
12046. .12129,12315. .12430,12535. .12636,12715. .12828,
12916. .12972,13222. .13288,13356. .13409,13798. .13872,
13956. .13991,14389. .14490)
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SPASPRSGRREAGGEGSGGGRAPYINVTRRSRRFWRDSSGGRDHAASREDSIHT
SPRSGRREAGGEGSGGGGRAPYINVTRRSRRFWRDSSGGRDHAASREDSIHT
SERTINNNGATIKLRPTENGTREFRCCRPSLVYTPINAGILGCHLCVLARLLCLRQGRWR
RHAARHAVRNEALGYVVVLRHYPSPVAATWRRRKQCATGALLPRYEAHTIEWTIGE
GEEEHDVRQPPGGGLRTLRLHQOPRRYESTSCARIGGGSRAGEKHPTLNCQHQRHDRT
TDDATVRWTTLKRKTTCARSVCHGRVQVWVQAPYQG"
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/db_xref="G1:2016135"
/db_xref="G1:201613
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/db_xref="G1:20161353"
/db_xref="G1:2016135
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AVKQHATYRQHQAIEGVNGCGAGGYNYNRHQAVAVAGGQHHYGGATAAAYGNASNKO
HFTAAAAGHHSSGGHTQYHHQSYECEEEDSDEDDDCEDDDDDESDDDDGHCPPSRQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KGAEGLAPGIVVPETDLYLRRLWGEPSEDLTSQPRYLITFTYGYSQRANIDAAVKKFS
ENFTIMLEHYDGRINDWDEFEWSKRAIHVSVRRQTKWWYAKRFLHPDIVAPYDYIFIW
DEDLSVQHFNAEAYIKLVRKHGLEISQPGLEPDKGLTWQMTKRLGDQEVHKYTEERPG
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22387. .22505,22923. .23035,23239. .23318))
/gene="P0470A12.3"
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22387. .22505,22223. .23035,23239. .23318))
/gene="P0470A12.3"
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VTKLHFPSSIISYIEDKDSGITTQTLLNHAMTSANSKKRNNSESNSDEIPKIYVPTNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WCTDPHLPPCAAFVELMATVFSRDAWRCVWHMIQNDLVHGWGLDFALRRCVEPAHEKI
GVVDSQWVIHQVIPSLGNQGTAENGRTPWEGVRARCRKEWGMFQKRLADAEKAYYLGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similar to Oryza sativa chromosome 5, P0574H01.
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/gene="P0470A12.2"
/note="contains_EST_AU069076(C51993)
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/gene="P0470A12.4"
/note="hypothetical protein"
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complement(23929, .24237)
/gene="P04/10A12.4"
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/gene="P0470A12.2"
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/gene="P0470A12.5"
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Direct Submission

AL Shamited (21-Mar-2001) Takuji Sasaki, National Institute of
Direct Submission

Direct Submission

Direct Submission

Direct Submission

Direct Submission

Sibmitted (21-Mar-2001) Takuji Sasaki, National Institute of
Agrobiological Sciences, Rice Genome Research Program; Rannondal

2-1-2, Tsukuba, Ibaraki 305-8602, Japan

2-1-2, Tsukuba, Ibaraki 305-8602, Japan

Cermalitzaaskienias affrec 100. The Journity (2011)

Tel:81-298-38-7441, Fax:81-298-38-7468)

On Oct 17, 2001 this sequence version replaced gi:13430001.

Genes were predicted from the integrated results of the following:
GENSCANI.0, BLASTNZ.0, BLASTNZ.0 as well as SplicePredictor
(October 1998 version). The genomic sequence was searched against
NEDI NonRedundant Protein database, nr

(ftp://ncbi.nlm.nih.gov/blast/db) and the CDNA sequence database at

(ftp://ncbi.nlm.nih.gov/blast/db) and the CDNA sequence database at

(ftp://ncbi.nlm.nih.gov/blast/db) and the CDNA sequence database at

(ftp://ncbi.nlm.nih.gov/blast/db) and the CDNA sequence database with BLASTP2.0. ESTS represent

NGF Protein homologies of the coding regions were searched against

NGF Protein homologies of the coding regions were searched against

NGF Protein homologies of the coding regions were searched against

Agene with identity or significant homology to a protein is

classified based on the protein name to indicate the homology (covering

significant homology to any protein name to indicate the homology to a significant homology to any protein homology to any protein name to indicate the homology to any protein name to indicate the homology to any protein name to indicate the homology to any protein of the sequence is from Sp6 to 77 of the PAC clone. The orientation of the sequence is from Sp6 to 77 of the PAC clone. Detailed information on overlap and assembly quality together with annotation/Onalifiers

Nurce //cgn.layGenomeseq.html.

1. 185095

Agene with identy is available at

Norganism="Originassing" database a
                                                               Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, PAG Colone:P0470A12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16232 AACGACTACCTGATGGTGGGGGAGGAGGAGGAGGACTTCAACACCTGCACGGC 16291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 GlyHisGlyPheValValArgGluThrArgValGluGluAspIleAsnThrCysThrGly 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA,
clone:P0470A12.
                                                                                                                                                                                                                                                                          20 AladlyPheGlyArgHisGlyGlyValGlnGlnHisValValValLysGluLysPheGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40 GluValAspThrValSerArgAlaGlyAlaAsnHisHisHisHisGlyHisHisGly
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Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0470A12
Published Only in Database (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16292 GAGTTCCGCGAGCGCAAGCAGAGCTTCCTGCTCAAGTCCGAC 16333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GluValHisGluArgArgGluSerPheLeuAlaArgAlaAsn 93
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CDS

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AC091088

*** SEQUENCING IN PROGRESS ***, 4 ordered pleces.

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AC091088.

AC091088.

GI.3487944

HTG. HTGS_PHASE2.

Oryza sativa (japonica cultivar-group).

SM Oryza sativa (japonica cultivar-group).

SPERMATYOTA: VITIdiplantae: Streptophyta; Embryophyta; Tracheophyta; Ehrhartoideae: Oryzea.

Ehrhartoideae: Oryzeae: Oryza.

Electrologicae: Oryza.

S. Lee, J.-S., Hahn, J.-H., Yoon, U.-H., Lee, M.-C., Yun, D.-W., Kim, H.-I.

and Eun. M., Hahn, J.-H., Yoon, U.-H., Lee, M.-C., Yun, D.-W., Kim, H.-I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27454 GGCGGCTTCCTCCGCCGCGCGCGCGCGCACCACCACCACCTCCACGAGACGTCCAG 27395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27343 AACGACTACCTGATGGTGCGGAGACCAAGGTGGAGGAGGACTTCAACACCTGCACCGGC 27284
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clone P0470A12,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39
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                                 complement(join(47978. ,48061,48179. ,48239,48314. ,48374,48478. ,48759,48374. ,49298. ,49552. ,49625,49763. ,49964,50111. ,50213,50317. ,50378,50507. ,50561,50738. ,50841,50926. ,51048,51175. ,51219,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 1111 ::::::: 27283 GAGTTCCGCGAGCGCAAGCAGCTTCCTGCTCAAGTCCGAC 27242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GluValHisGluArgArgGluSerPheLeuAlaArgAlaAsn 93
                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                      Gaps:
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                                                                                                                                                                                                                   3.29e-17
295.00
75.53%
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Best Local Similarity:
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JOINT(40309, 40472, 40627, 40622, 40913, 41002,41120, 41176, 41290, 41359,41646, 41710,42307, 42361,42603, 42730, 42818, 42906,43104, 43179,43072, 43361,42603, 43730, 43983, 444311,44519, 44650,44113, 44799,46231, 46311, 46311, 46380, 46604,46714, 46636,46920, 47036)

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JOHN (40300, 4070,40714, 46836,46920, 477036)

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PFSKFGFKREYTLSGRYDLELAVGDAAMENSFLRALGHIELDDLEAAPRERAKPPRAQAVD
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                                                                                                                                                                                                                                                 /translation-"MOSGGTASPAGVAGDGAGGRGSVFRGDDAPKLLAALKEMKEGLD
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FLGRGGVQDHVVKETFQEIDRSGSGRHHHNNHGNDYLMVREIKVEEDFNTCTGEFR
ERKQSFLLKGD"
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ement(join(27239. .27499,30542. .30622,30720. .30899,
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              SST242802 562 bp mRNA linear PLN 27-NOV-1999 Sporobolus stapfianus mRNA for putative glycine-rich protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sporobolus stapfianus.
Spermatophyta: Magnoliophyta: Liliopsida: Poales: Poaceae; PACC.
Lade; Chloridoideae; Eragrostideae; Sporobolus.
(bases 1 to 562)
Neale, A.D., Bromstedt, C.K., Bromson, P., Le, T.N., Guthridge, K.,
Sprans, J., Gaff, D.F. and Hamill, J.D.
The isolation of lowly-transcribed genes which are induced during dessication of the resurrection grass Sporobolus stapfianus
                                                                                                                                                                                                                                                                                                                                                                                                                                          40 GluValAspThrValSerArgAlaGlyAlaAsnHisHisHisHisHisGlyHisHisGly 59
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Submitted (27-MAX-1999) Neale A.D., Biological Sciences, Monash
University, Wellington Rd Clayton, Victoria, 3168, AUSTRALIA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                     20 AlaGlyPheGlyArgHisGlyGlyGlyValGlnGlnHisValValLysGluLysPheGlu
                                                          1. .185481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              374 others
138783: contig of 45331 bp in length 4 138883: gap of unknown length 4 185481: contig of 46598 bp in length. Location/Qualifiers
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57
14
19
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    .562
    .502mism="Sporobolus stapfianus"
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Mismatches:
Indels:
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41522 c 41493 g 50653 t
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AJ242802.1 GI:6478143
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sinorhizobium meliloti.
Sinorhizobium meliloti
Bactoria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
1 (bases 1 to 30000)
Capela,D., Barloy-Hubler,F., Gouzy,J., Bothe,G., Ampe,F., Batut,J.,
Solistard,P., Becker,A., Boutry,M., Cadleu,E., Dreano,S., Gloux,S.,
Godrie,T., Goffeau,A., Kahn,D., Kiss,E., Lelaure,V., Masuy,D.,
Pohl,T., Portetelle,D., Puehler,A., Purnelle,B., Ramasperger,U.,
Renard,C., Thebault,P., Vandenbol,M., Weidner,S. and Galibert,F.
Analysis of the chromosome sequence of the legume symbiont
Sinorhizobium meliloti strain 1021
Droc. Natl. Acad. Sci. U.S.A. 98 (17), 9877-9882 (2001)
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Submitted (26-JUL-2001) Gouzy J., Submitted on behalf of the MELILO
EU Consortium
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                                                                                                                        /translation="MAHFREWDY EBVTSMAKPGFGRHGGGGVQOFVVKETFEEVEQV TPRGRSGHHGGHRGNGGHGSCHFQARETKFERHQHAHRRVPRAGGERPCGG" 153 c 154 g 112 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GluGluValAspThrValSerArgAlaGlyAlaAsnHisHisHisHisHisGlyHisHis 58
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Indels:
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Matches:
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225.50
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59.00%
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/codon_start=1
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LDDABIAAYIPGEKHGTREFYEBERILAAGCKDSGADVIRAAVSDEKQDFSKCVAVRK
DGWAVDIDGDYTETLARIASNKNGIGVFGLSFYENNADKLKVATVMGIVPGTETIASG
EPVVSKRAHIGVIPGLKEYVEFFVDDQMIGPDSPLAEYGLVAAPDAEREEI
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AVVLLVSVAGGLYAIRNIDVRFRAAIGWSASCSARSSSPRP"
Universite Catholique de Louvain, Place Croix du Sud 2, Bte 20, B-1348 Louvain-la-Neuve, Belgium, Unite de Microbiologie, Faculte des Sciences Agronomiques de Gembloux, Avenue Marechal Juin 6, B-5030 Gembloux, Belgium. E-mail:Jerome.Gouzy@toulouse.inra.fr http://sequence.toulouse.inra.fr
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                                                                                                                                                                                                                                                                                                                                                                                                         small molecules"
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1241. .1846
/gene="SMc02145"
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/function="product confidence : hypothetical
gene name confidence : hypothetical
predicted by Codon_usage
predicted by FrameD"
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/gene="pstC OR SMC02144"
1813. 2724
/gene="pstC OR SMC02144"
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Gene name confidence: purpage
predicted by Codon_usage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear PLN 27-JUL-1997 protein RAP2.10 mRNA,
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
alaokvisddtilddaeroigekalvtiakropmasdlreimgsirlaadlervgdlg
Kntakrviavagsgiprklarglehlaelalvolkevldvyaskspekansirerdeb
Idaiytslerelliymmedprnitpcthllecaknierigdhatniaetiyymatgao
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 ArgSerValAlaProAlaGlyPheGlyArgHisGlyGlyValGlnGlnHisValVal 34
                                                                                                                          /function="small molecule metabolism; global functions; global regulatory functions"
/note="predicted by Codon_usage
                                                                                                                                                                                                                                          /product="PHOSPHATE REGULON TRANSCRIPTIONAL REGULATORY PROTEIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LysGluLysPheGlu-----GluValAspThrValSerArgAlaGly-----
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Okamuro,J.K., Caster,B., Villarroel,R., Van Montagu,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jofuku, K.D.
The AP2 domain of APETALA2 defines a large new family of
binding proteins in Arabidopsis
Proc. Natl. Acad. Sci. U.S.A. 94 (13), 7076-7081 (1997)
97338147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 ThrArgValGluGluAspIleAsnThrCysThrGlyGluValHisGluArg 84
                                                                                                                                                                                                                                                                                                                                                              300000
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Arabidopsis thaliana AP2 domain containing partial cds.
                                                                                                                                                                                                                                                                                                                                                                                          Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                /protein_id="CAC45087.1"
/db_xref="G1:15073445"
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Matches:
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                                                                  5783. .6466
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5783. .6466
/gene="phoB OR SMC02140"
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predicted by FrameD"
                                                     PQGERPKDDMTSTLGSVTD"
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AF003103.1 GI:2281644
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Arabidopsis thaliana
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39.18%
28.87%
18.33%
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DEFINITION
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Arabidopsis thaliana.
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                     Santa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53 HisHisHisGlyHis---HisGlyGlyHisGlyPheValValArgGluThr----Arg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (1. 781
/note="putative DNA binding protein; similar to A.
thaliana APETALA2 encoded by GenBank Accession Number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 815).

(bases 1 to 815).

(clerryn, N. Heijnen, L., Ge Keyser, A., Van Asseldonck, M., Decreryn, N., Vetlankel, H., Gielen, J., Zabeau, M., Villarroel, R., Jesse, T., Neyt, P., Hogers, R., Van Den Daele, H., Ardiles, W.,
                                                                                                                                                                                                                                                                                                                                                                                                                'note="similar to EST with GenBank Accession Number
                                                              Offuku.K.D.
Direct Submission
Submitted (08-MAY-1997) Biology, University of California,
Cruz, CA 95064, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=2
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2 (bases 1 to 814)
Okamuro,J.K., Caster,B., Villarroel,R., Van Montagu,M.
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Arabidopsis thaliana mRNA for TINY-like protein.
AJ002598
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177
177
177
177
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                               /organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
1. .814*
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/note="encodes AP2 domain"
/note="encodes AP2 domain"
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92.50
50.70%
33.80%
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Query Match:
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Cheuk, R., Chen, H., Kim, C.J., Koesema, E., Meyers, M.C., Banh, J.,
Buwser, L., Carninci, P., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y.,
Buwser, J., Carninci, P., Jones, T., Kamiya, A., Karlin-Neumann, G.,
Ishida, J., Lam, B., Lee, J.M., Lih, J., Liu, S.X., Miranda, M.,
Ravai, J., Lam, B., Lee, J.M., Lih, J., Liu, S.X., Miranda, M.,
Raviska, M., Mayven, M., Onodera, C.S., Palm, C.J., Pham, P.K.,
Ouach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C.,
Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K.,
Davis, K.W., Theologis, A. and Ecker, J.R.
Submitted (24-SEP-2001) Salk Institute Genomic Analysis Laboratory
Kignaki, Plant Biology Laboratory, The Salk Institute for
Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
                                            Spermatophyta; Magnollophyta; endloctyledons; core eudlocts; Roslades; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

Cheuk,R., Chen,H., Kim,C.J., Koesema,E., Meyers,M.C., Banh,J., Bowser,L., Carninci,P., Dale,J.M., Goldanith,A.D., Hayashizaki,Y., Rawai,J., Lam,B., Lee,J.M., Lin,S.X., Marlada,M., Marga,P.X., Jones,T., Kanin,A.Z., Marlada,M., Nauyen,M., Ondera,C.S., Palm,C.J., Pham,P.K., Ouach,H.L., Sakurai,T., Satou,M., Seti,M., Seti,M., Seti,M., Southwick,A., Tang,C.C., Dalais,R.W., Theologis,A. and Ecker,J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL CDNAS: Cheuk.R., Chen,H., Klm,C.J., Koesema,E., Meyers,M.C., Shinn,P., Banh,J. Bowser,L., Dale,J.M., Goldsmith,A.D., Jiang,P.X., Jones,T., Karlin Neumann,G., Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M., Nguyen,M., Onodera,C.S., Palm,C.J., Pham,P.K., Quach,H.L., Southwick,A. Tang,C.C., Toriumi,M., Yamada,K., Yamamura, Y., Yu,G., Yu,S., Davis,R.W., Theologis,A., and Ecker,J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="AT4g36900/C7A10_460"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAS (RAFL cDNA : 'RIKEN Arabidopsis Full-Length cDNA') : Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                  Embryophyta; Tracheophyta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1009
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/organism="Arabidopsis thaliana"
/db_aref="taxon:3702"
/chromosome="4"
                           Eukaryota; Viridiplantae; Streptophyta;
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/note="ecotype: Columbia"
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/note="TINY-like protein"
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Pred. No.:
                                                                                           REFERENCE
                                                                                                                    AUTHORS
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REFERENCE
AUTHORS
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                                                                                                                                                                                 Terryn, N. S. E.

S. Terryn, N. S. E.

Direct Submission

L. Submitted (14-NOV-1997) Terryn N. S. E., Genetics, Flanders
Interuniversity institute for biotechnology, K. L. Ledeganckstraat
35, 9000 Gent. BEGIDM

this CDNA is corresponding to EST 140D13 (T76017).

I. Cortion/Qualifiers

1. 615

/organism="Arabidopsis thaliana"
/db_xref="Exazon:3702"
//map="93.cM"
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/tasslation="FFETSSLLRFRVPLLSSWPTCSSISPSACNRFAVNITSFFFIF

KISLDRFFCGFLKSPERTTMETATETATEVATVVSTPAVTVAAVATEKRDKPYRGJFRMRKWG
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GGGGVNGGDMSAAYIRRKAAEVGAQVDALERAGGGRHHHHHHQQRGNHDYVDNHS
DYRINDDLMECSSKRGFKRCNGSLERVDLNKLPDPETSDDD"
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Schueller, C., Mayer, K., Dehais, P., Rombauts, S., Van Montagu, M., Rouze, P. and Vos, P.
Evidence for an ancient chromosomal duplication in Arabidopsis thaliana by sequencing and analyzing a 400-kb contig at the APETALA2 locus on chromosome 4
FEBS Lett. 445 (2-3), 237-245 (1999)
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/product-"133 q 212 t
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Stover C.K., Pham.X.Q., Erwin, A.L., Mizoguchi, S.D., Warrener, P., Stover, C.K., Pham.X.Q., Erwin, A.L., Mizoguchi, S.D., Warrener, P., Hickey, M.J., Brinkman, P.S., Hifnagle, W.O., Rowallk, D.J., Lagrou, M., Garber, R.L., Goltry, L., Tolentino, E., Westbrock, Wadman, S., Yaun, Y., Smith, K., Spencer, D., Wong, G.K., Wu, Z. and Paulsen, I.T. Complete genome sequence of Pseudomonas aeruginosa PA01, an Opportunistic pathogen
Nature 406 (6799), 959-964 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stover, C.K., Pham, X.-Q.T., Erwin, A.L., Mizoguchi, S.D., Warrener, P., Stover, C.K., Pham, X.-Q.T., Erwin, A.L., Mizoguchi, S.D., Warrener, P., Hickey, M.J., Brinkman, F.S.L., Hufnagle, W.O., Kowalik, D.J., Hickey, M.J., Brinkman, F.S.L., Tolentino, E., Westbrook, Wadman, S., Yuan, Y., Brody, L.L., Coulter, S.N., Westbrook, Wadman, S., Yuan, Y., Brody, L.L., Coulter, S.N., Folger, K.R., Kas, A., Larbig, K., Lim, R.M., Smith, K.A., Spencer, D.H., Wogg, G.K.-S., Wu, Z., Paulsen, I.T., Reizer, J., Saier, M.H., Hancock, R.E. W., Lory, S. and Olson, W.V.
Direct Submission Lory, S. and Olson, W.V.
Direct Submission Genome Center, University of Washington, University of Washington Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10757 bp DNA linear BCT 30-AUG-2000 PA01, section 122 of 529 of the complete
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                                                                                                                                          GlyPheGlyArgHisGlyGlyGlyGlyGlyGlnGlnHisValValLysGluLysPheGlu 39
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Pseudomonas aeruginosa
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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product_probable MFS transporter"
/protein_id="AAG04705.1"
/db_xref="GI:9947254"
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/organism="Pseudomonas aeruginosa"
               Conservative:
Mismatches:
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110. .1651
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/gene="PA1316"
110. 1687
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GLGEFARTGWNAY PELSELAYSPGGGVGVDY I WALLOJGSGMGTLLYGINFLYVFKMRTP
GMKLMOMPI FFWTCTPANILJYASPPILTALIGLIGLBRYLDMHFFWIEDGGNAMMYI
NEWAMGGBPEVILLIPAFGISEVTATFAGKRMFGYKSWWASAAITFGFFTAFGTKRWFT
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IGGMTGVLLAIPGADFLLIANSLFILTHFHNIIGGRAFGYFTAGFTLDE
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MKKAGTARYKLPAYOPIHMPKNTAAGFSIAVFAFFGFAAIMHWMLMAVGFVGMLGS
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FASVFATYAVLVHHTAGGPSGKDIFELPYVLVETAILLVSSCTYGLAMLSAHKGAKGG
AIAWLGVTFLLGAAFIGWEINEFHHLIAEGFGPSRSAFLSSFFTLVGAHGLHVSAGLL
WMLVLMAQIWTRGLTAQNNTRWMCLSLFWHFLDIVWICVFTVYYLMGAL"
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EGGWLSPTAWPALLLAGVGLIGFLFVERRTARPLLPLGIFAGGRAVCNLASFYLGFS
GYASILFEISLFROQVQGASAQOAGFTATAPDFIAMAGALSMLFGRLQRHVPLRRLLVLGY
LVIGLAMLAGAGGTGTAYPWGLLIVALGIGAGIAVPGTGIAVMASYARERSGMASA
TWNTLRQAGMAVGILLGALLSGRAIVVLGDRLBGLGIADAQRIATQAVTAHRLPGSL
AGIDAELPAALABGFRLAMLVAGASALLAAALLWRLRVSAGPAADTVGASGRFRGVQL
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WTEWLTSVDHKKIGVMYIVVALVMLVRGFADAIMMRGQLALAEGANHGYLPPEHYDOI
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RAVQGIAGALLIPGALSILTQAFHDPGQRAQVIGGWTSFSALSLILGPLLGGLLVFHA
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5260. .5889
/gene="cyoc"
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3280. .5256
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/gene="cyoD"
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Direct Submission

La Submitted (10-MAR-2000) MIPS, at the Max-Planck Institut fuer
Blochemie, Am Klopferspitz 18a, D-82152 Martinaried, FRG, E-mail:
Blochemie, Am Klopferspitz 18a, D-82152 Martinaried, FRG, E-mail:
lemcke@mlps.blochem.mpg.de_mayeremlps.blochem.mpg.de project
Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge
Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK,
E-mail: michael.bevanebbarc.ac.uk
Information on performance of analysis and a more detailed
annotation of this entry and other sequences of chromosomes 3, 4
and 5 can be viewed at: http://www.mips.blochem.mpg.de/proj/thal/
this fragment has an overlap with ATCHRIV8S at the 5' end and an
overlap with ATCHRIV87 at the 3' end.

Location/Qualifiers

ree
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ALI61590.2 GI:7270623
                                                                                                                                                                           6104 CGACAT------GTTCATGTG------CAGGAAGCAGATCAG 6075
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VEATLYRVPETLSQEVVEQMKAPVKDLEIPEITAAELTAADGFLFGFPTRYGGMAADM
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FGAGMFKMDSIRGGSPYGAGVFAGDGSREATETELALAEHQGNYMAAIVKRLAQP"
                                                                                                                                         4 TyrGlnGluValAspTyrCysSerGluGluValArgSerValAlaProAlaGlyPheGly 23
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Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta: Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicalas; Brassicaceae; Arabidopsis,
1 (bases 1 to 198780)
EV Arabidopsis, sequencing, project.
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                                                                                                                                                                                                                                                                                                                                      44 ValSerArgAlaGlyAlaAsnHisHisHisHisHis-----GlyHisHisGlyGly
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Gaps:
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DB:
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DEFINITION
ACCESSION
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ORGANISM
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ATCHRIV86
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AUTHORS
TITLE
JOURNAL
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KEYWORDS
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Best Local Similarity:
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MPRarpleamcrardevgkildpss"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contains Cytochrome P450 cysteine heme-iron ligand signature [FGLGRRACPG]"
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Submitted (29-JUL-1999) MIPS, at the Max-Planck-Institut fuer
Submitted (29-JUL-1999) MIPS, at the Max-Planck-Institut fuer
Submitted (29-JUL-1999) MIPS, at the Max-Planck-Institut fuer
Bloochemie, Max Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:
Schuelle@mips.blochem.mpg.de.mayer@mips.blochem.mpg.de Project
Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge
Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK,
On Mar 7, 1999 this sequence version replaced gi:4006849.
Information on performance of analysis and a more detailed
annotation of this entry and other sequences of chromosomes 3, 4
and 5 can be viewed at: http://www.mips.blochem.mpg.de/proj/thal/
this fragment.has an overlap with ATAP22 at the 3' end.
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Arabidopsis thaliana
Eukaryota; Viridiplantue; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
I (bases 1 to 206420)
Bevan, M., Terryn, N., Vos, P., Heijnen, L., Mewes, H.W., Mayer, K.F.X.
                                                                                                                                                                                                                                                                                                                                                                    21 GlyPheGlyArgHisGlyGlyGly---ValGlnGlnHisValValLysGluLysPheGlu 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                 40 Glu------AsnHisHis 52
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Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment
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Matches:
Conservative:
Mismatches:
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EU Arabidopsis sequencing, project.
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299707
299707.1 GI:4376087
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50.70%
33.80%
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Best Local Similarity:
Query Match:
DB:
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KEYWORDS
SOURCE
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Contains ATP/GTP-binding site motif A (P-loop) [ARAIVGKT],
Cytochrome P450 cysteine heme-iron ligand signature
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978. . 1475
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
I (bases 1 to 1898)
Bariharan, N., Kelley, D.E. and Perry, R.P.
Hariharan, N., Kelley, D.E. and Perry, R.P.
Belta, a transcription factor that binds to downstream elements in several polymerase II promoters, is a functionally versatile zinc finger protein
Proc. Natl. Acad. Sci. U.S.A. 88 (21), 9799-9803 (1991)
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/translation="MDLTQILLLSFLFLTISIKLLLTKSNRKPNLPFSPAYPLPVIGH
LHLLKQPVHRTFHSISKSLGNAPIFHLRLGNRLVYVISSHSIAEECFTKNDVVLANRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53 HisHisHisGlyHis---HisGlyGlyHisGlyPheValValArgGluThr-----Arg 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40 Glu------AsnHisPThrValSerArgAlaGlyAla-----AsnHisHis
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Mouse delta transcription factor mRNA, complete cds.
M74590
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/db_xref="taxon:10090"
43. .1287
/standard_name="delta"
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1. 1898
/organism="Mus musculus"
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6495..6879
/gene="C7A10.40"
/number=1
6880..7263
/gene="C7A10.40"
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us-10-090-035-2.rge

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'function="MuLV UCR-motif DNA-binding protein"
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                                    /codon_start=1
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/gene="UCRBP"
2301 . 2306
/gene="UCRBP"
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92.00
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Best Local Similarity:
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MUSTRANS01
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TITLE
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KEYWORDS
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/product="delta-transcription factor"
/product="delta-transcription factor"
/protein_id="AAA37521.1"
/protein_id="AAA37521.1"
/protein_id="192941"
/protein_
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Flanagan, J.R., Becker, K.G., Ennist, D.L., Gleason, S.L., Clanagan, J.R., Becker, K.G., Appella, E. and Ozato, K.
Cloning of a negative transcription factor that binds to the upstream conserved regain of Moloney murine leukemia virus 92107191
1309593
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Mus musculus UCR-motif DNA-binding protein (UCRBP) mRNA, complete
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22
7
26
16
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Matches:
Conservative:
Mismatches:
Indels:
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DNA-binding protein; zinc-finger protein.
Mus musculus cDNA to mRNA.
Mus musculus
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                                                                                                                                                                                                                                        KFAQSTNLKSHILTHAKAKNNO"
453 c 525 g 4.
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/gene="UCRBP"
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/gene-"UCRBP"
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40.858
30.998
118.048
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Best Local Similarity:
Query Match:
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Mouse delta/YY1/NF-E1/UCRBP transcription factor, exon 1. L13969 L13969.1 GI:293843
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 GlyPheGlyArgHisGlyGlyGlyValGlnGlnHisValValLysGluLysPheGluGlu 40
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Safrany, G. and Perry, R. P.
Characterization of the mouse gene that encodes the delta/YXI/NF-EI/UCRBP transcription factor
Proc. Natl. Acad. Sci. U.S.A. 90 (12), 5559-5563 (1993)
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Mus musculus
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1 of 5
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Mismatches:
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/dev_stage="4-6 weeks"
/tissue_lib="1295V Stratagene"
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61 HisGlyPheValValArgGluThrArgValGluGluAspIleAsnThrCysThrGlyGlu 80
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Conservative:
Mismatches:
Indels:
Gaps:
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|||||| :::||| :::
2501 GTGCACCACCAGGAGGTGATCCTGGTGCAG 2533
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1776. 2885
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us-10-090-035-1\_1.rst

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/note="Organ: tassel, kernal, silk, husk, root, leaf;
Vector: pGAD10; Site_1: EcoRI; cDNA library from fully
differentiated maize tissues from an active Mutator plant.
Tissue ratio is 4:2:1:1:11 (tassel, kernel, silk, husk,
root, leaf). Unidirectionally cloned. New library number
given to library 707 for additional sequencing."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 GACACACCAAGCGTCTGCACCAATGGCTTACTACCAGGAGGTGGACTACTGCTCGGAGGA 126
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              Contract: Walbot v
Contract: Walbot v
Contract: Walbot v
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: Walbotestanford.edu
Plate: 945002 row: E column: 06.
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Job time : 1458.61 secs

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC clade: Panicoideae; Andropogoneae; Zea.

Maize ESTs from various cDNA libraries sequenced at Stanford

Walbot, V

REFERENCE AUTHORS TITLE

FEATURES

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Locations mays"

/organism="Zea mays"
/cultivar="B73"
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/clone_lib="603 - stressed root cDNA library from
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/lab_host="E. coli XL Gold"
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/note="Organ: root; Vector: root;
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                                     USA
Department of Biological Sciences Stanford University 855 California Ave, Palo Alto, CA 94304, USP Tel: 650 723 2227
Fax: 650 725 8221
Email: walbockstanford.edu
Plate: 603016 row: F column: 02.
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Pred. No. 2.9e-41;
0; Mismatches 8;
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les 488; Conservative
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603016F02.x1 603 - stressed root cDNA library from Wang/Bohnert lab
Zea mays cDNA, mRNA sequence.
AI855425
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1; Poales; Poaceae; PACC
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[ bases 1 to 539]
Walbot,V.

Maize ESTs from various CDNA libraries sequenced at
                                                                                                                                                                                                                                       68.5%; Score 462.8; DB 12; Length 96.8%; Pred. No. 1.4e-41; ive 0; Mismatches 13; Indels
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Sukaryota; Magnollophyta; Liliopsida; Poales; Poaceae; PACC clade; Pantcoideae; Andropogoneae; Zea.

I (bases I to 550). L., Ashlock, D.A, Wen, T.J. and Schnable, P.S.

Expressed Sequence Tags from B73 Malze Seedlings and Silks

Unpublished (2001)

on May 25, 2001 this sequence version replaced g1:14206705.

Contact: Patrick S. Schnable

Contact: Patrick S. Schnable

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Iowa State University

G405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA

Tel: 515-294-0975

Fax: 515-294-2299

Email: schnable@lastate.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BG840383 550 bp mRNA linear EST 29-MAY-2001
MEST12-H11.T7-1 ISUM4-TN Zea mays CDNA clone MEST12-H11 5', mRNA
                                    104 GGTGAGGTCGGTGGCCCCGGCCGGCTTCGGCCGCCACGGAGGCGGCGTCCAGGAGCACGT 163
                                                                                                                                                                          304 GGACATCAACACCTGCACCGGCGAGGTCCACGAGCGAGGGAGAGCTTCCTCGCCAGGGC 363
                                                                                                                                                                                               /note="Vector: pT7T3PAC; Site_1: EcoRI; Site_2: NotI; ds-cDNA molecules were generated as follows. First-strand cDNA was prepared from oligo-dT selected mRNA by priming with a NotI oligo-dT primer (5'
                                                                                                      244 CCACCACCATGGTCACCACGGCGACGCTTCGTGGTGCGCGAGACCAGGGTCGAGGA
                                                                                                                                                                                                                                                                                                                     424 TATGTCTGTGGTTGACTGGTTGTGCAGGGTCATCGTACTTGGCTATCGTACGTGCACGCA
                                                                                                                                                                                                                                                                                                                                                                                           CTCAGCTCCTGTACGAATTACGACAATAAGCTCGTGACCTGAATAAAACTTCTTCGTAAT
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BACKWARD: T3 (ATT AAC CCT CAC TAA AG)
Seq primer: primer T7-1 (AA TAC GAC TCA CTA TAG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="ISUM4-TN"
/tissue_type="Seedling and silk"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:4577"
/clone="MEST12-H11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 544 ACTAATACCTACATCAAAAAAA 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     524 AAAAAAAAAAAAAAAAAA 546
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/cultivar="B73"
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//tissus_type="above ground tissues"
//tissus_type="above ground tissues"
//dev_statge="Two.leaf.stage green seedling"
//dev_statge="Two.leaf.stage green seedling"
//dev_statge="XL1-MFR Blue"
//note="Organ: green seedlings; Vector: pAD-GAL4; Site_1:
ECORI; Site_2: Xho!; ds-CDNA molecules were generated as
follows. First-strand CDNA was prepared from oilgo-dT
resulting DNA:RNA hybrid was treated with RNase H and used
synthesis. After the addition of EcoRI adaptors, the
ds-CDNAs were digested with XhoI and size-selected. The
resulting molecules were directionally cloned into the
ECORI and XhoI sites of the Hybrizap lambda vector
(Stratagene) and excised as PAD-GAL4 phagemids."
30 a 168 c 159 g 88 t longered.
                                                                                                                                                                                             AA779839
MEST2-B7.TW1412.Seq ISUM2 Zea mays cDNA clone MEST2-B7 5', mRNA
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Zea.

1 (bases 1 to 546)
Wen,T.J., Ashlock,D.A. and Schnable,P.S.
Wen,T.J., Ashlock,D.A. and Schnable,P.S.
Unpublished (1997)
Contact: Schnable, PS
Schnable laboratory
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                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FORWARD: tw1412 (5'-GAAGATACCCCACCAAACC-3')
BACKWARD: T7-YJ (5'-TAATACGACTCACTATAGGCC-3')
Plate: WEST2 row: B column: 7
Seq primer: tw1412 (5'-GAAGATACCCCACCAAACC-3')
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Iowa State University
6405 Agronomy, Ames, IA 50011, USA
Tel: (515)-294-0975
Fax: (515)-294-2299
Email: Schnable@iastate.edu
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/clone="MEST2-87"
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/cultivar="B73"
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/note="Organ: tassel, kernal, silk, husk, root, leaf; 
Vector: pGAD10; Site_1: ECORI; cDNA library from fully 
differentiated maize tissues from an active Mutator plant. 
Tissue ratio is 4:2:1:1:1:1 (tassel, kernel, silk, husk, 
root, leaf). Unidirectionally cloned. New library number 
given to library 707 for additional sequencing."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A linear EST 16-MAY-2000 from Walbot lab, same as 707
                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea. 1 (bases 1 to 500) Walbot, V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATCAACACCTGCACCGGCGAGGTCCACGAGCGCAGGGAGAGCTTCCTCGCCAGGGCTAA
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/organism="zea mays"
/outhivar="W23"

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                                                                                                                                                                                                                                                                                                        Maize ESTs from various cDNA libraries sequenced at
                                                                                                                                                                                                                                                                                                                                                                                    Department of Biological Sciences
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USi
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stenford.edu
Plate: 945002 row: E column: 06.
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Pred. No. 2.2e-42;
                                                               tissues
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                                                                     (SK) Zea mays cDNA, mRNA sequence.
                                           500 bp
adult t
                                                               945002E06.X3 945 - Mixed
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                                                                                                                            AW787732.1 GI:7844510
                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
Contact: Walbot V
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Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                          /note—"this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25 GCAGCAATCCACACAAGCACTTCGAAGGACCACTG-----CTCGGAGGACACACCAAGCG
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                                                                          of
                                                                                                                                                                                                                                                                                                                              /clone_ibc0124784"
/clone_lib="Maize Mapping Project/DuPont Cornsensus
Library"
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                                1 (Dases 1 to 303)
Arthur,L.W., Hanafey,M., Mao,G.H., Vogel,J.W., Whitsitt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design (Overgo Probes
Unpublished (2002)
2 (bases 1 to 553)
Coe,E.C.
                                                                                                                                                                                                        University
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                                                                                                                                                                                Submitted (25-APR-2002) Maize Mapping Project, Submitted (25-APR-2002) Maize Mapping Project, Missouri, Columbia, MO 62211, USA Location/Qualifiers 1.553
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Pred. No. 8.5e-43;
0; Mismatches 23;
clade; Panicoideae; Andropogoneae; Zea
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                                                                                                                                                                                                                                                                                    /organism="Zea mays"
/db_xref="MaizeDB:637271"
/db_xref="taxon:4577"
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173 c 162
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al Similarity 94.3%;
516; Conservative C
                       (bases 1 to 553)
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adult tissues from Walbot lab

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/organism="Zea mays"
/cultivar="W23"
/db_xref="taxon:4577"
/clone_lib="707 - Mixed
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       Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 707009 row: E column:
Location/Qualifiers
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/note="Organ: tassel, kernal, silk, husk, root, leaf; Vector: pGAD10; Site_1: EcoRI; cDNA library from fully differentiated maize tissues from an active Mutator plant. Tissue ratio is 4.2:1:1:1:1 (tassel, kernel, silk, husk, root, leaf). Unidirectionally cloned. New library number given to library 707 for additional sequencing."
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tissues from Walbot lab (SK) 2ea
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( Dases 1 to 524)
Walbot, V.

Walbot, V.
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                                                                                    Score 492.6; DB 10; Length 552;
Pred. No. 8.9e-45;
0; Mismatches 14; Indels 0;
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855 California Ave, Palo Alto, CA 94304,
Tel: 650 723 2227
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Contact: Walbot V
Department of Blological Sciences
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mmys cDNA, mRNA sequence.
                                                                                    72.9%;
llarity 97.3%;
Conservative
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/tissue_type="tassel, kernel, silk, husk, root, leaf"
/dev_stage="adult"
/dev_stage="adult"
/lab_host="bul08"
/note="Organ: tassel, kernel, silk, husk, root, leaf;
/note="Organ: tassel, kernel, cDNA library from fully
Vector: pGADIO; Site_1: EcoRI; cDNA library from fully
Vefferentiated maize tissues from an active Mutator
plant. Tissue ratio is 4/2/1/1/1/1 (tassel, kernel, silk,
husk, root, leaf). Unddirectionally cloned."
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
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0; Mismatches 14; Indels
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Zea mays PCO124784 mRNA sequence.
AY104409
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Local Similarity 96.5%;
Nes 503; Conservative (
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BE025302
945028B09.Yl 945 - Mixed adult tissues from Walbot lab, same as 707 (SK) Zea mays cDNA, mRNA sequence.
BE025302.1 GI:8318737
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/outline="W23"
/ob_xref="taxon:4577"
/clone_lib="945 - Mixed adult tissues from Walbot lab,
same as 707 (SK)"
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/dev_stage="fully-grown"
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                                                                                     GGTGAGGTCGGTGGCCCCGGCCTTCGGCCGCCACGGCGGCGGCGTCCAGCACGT
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/dlone_lib="707 - Mixed adult tissues from Walbot lab (SK

/dlone_lib="707" - Mixed adult tissues from Walbot lab (SK
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/dev_stage="adult"
/lab_host="DH10B"
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Pred. No. 2.3e-45;
0; Mismatches 8; Indels 0;
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University
Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 227
Fax: 650 728 8221
Email: walbot@stanford.edu
Plate: 707049 row: E column: 04.
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/organism="Zea mays"
/cultivar="W23"
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ilarity 98.4%;
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Zea mays
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BQ619390 648 bp mRNA linear EST 27-JUN-2002 RNOSEQ7B09_SK.abl Salt stressed Zea mays roots cDNA library Zea mays cDNA clone RNOSEQ7B09_SK.abl similar to No homology, mRNA
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1 (bases 1 to 648)
Wang, H. and Bohnert, H.J.
Genomics of plant stress tolerance
Unpublished (2002)
Contact: Mark Fredricksen
Department of plant Biology
University of Illinois
University of Illinois
Tel: 2172655473
              180 CGTCAAGGAGAAGTICGAGGAGGICGACAGGTCTCACGCGCGCGCGCCAACCACCA 239
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                                                Email: Art. 2003. A. Coation/Qualifiers

Location/Qualifiers
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/clone="RNOSEO7B09_SK.abl"
/clone="RNOSEO7B09_SK.abl"
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0; Mismatches 14; Indels
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/dev_stage="2 weeks old"
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Mang, H. and Bohnert, H.J.
Wang, H. and Bohnert, H.J.
Whouls of plant stress tolerance
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/tissue_type="Roots"
/dev_stage="2 weeks old"
/note="Vector: pBluescript SK+; Stressed 24 hours at 1
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Department of Plant Biology
University of Illinois
1201 W. Gregory Dr., Urbana, IL 61
Tel: 2172655673
Email: bohnertlab@life.uiuc.edu.

Location/Qualifiers
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BQ619337 648 bp mRNA linear EST 27-JUN-2002 RNOSEQ6E12_SK.abl Salt stressed Zea mays roots cDNA library Zea mays cDNA clone RNOSEQ6E12_SK.abl similar to No homology, mRNA
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Eukaryota, Varidiplantae; Streptophyta; Embryophyta; Poaceae; PACC
clade; Panicoldeae; Andropogoneae; Zea.
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Wang, H. and Bohnert, H.J.
Genomics of plant stress tolerance
Unpublished (2002)
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Pred. No. 1.5e-46;
0; Mismatches 14; Indels 3;
                                                                                                                                                                                                                                                                                                                                               Contact: Mark Fredricksen
Department of Plant Biology
University of Illinois
1201 W. Gregory Dr., Urbana, IL 61801, USA
Tel: 2172655473
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Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC
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Genomics of plant stress tolerance
Unpublished (2002)
Contact: Mark Fredricksen
Contact: Mark Fredricksen
Contactment of Plant Biology
University of Illinois
1201 W. Gregory Dr., Urbana, IL 61801, US:
Tel: 2172655473
Email: bohnertlab@life.uiuc.edu.
Location/Qualifiers
ce /organism="Zea mays"
// Organism="Zea mays"
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Matches 530; Conservative 0; Mismatches 14
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Wang, H. and Bohnert, H.J.
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                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 648)
Wang, H. and Bohnert, H.J.
Genomics of plant stress tolerance
Upubblished (2002)
Contact: Mark Fredricksen
Department of Plant Biology
                                 150
                                                                                                                                               CDNA library
                                                                                                                                                                                                                                                            /clone_lib-"Salt stressed Zea mays roots cDNA library
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/note="Vector: pBluescript SK+; Stressed 24 hours at
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                                                                            DB 14; Length 648;
                                                                       / Match 75.2%; Score 508.6; DB 14; Length
Local Similarity 96.9%; Pred. No. 1.5e-46;
nes 530; Conservative 0; Mismatches 14; Indels
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University of Illinois
1201 W Gregory Dr., Urbana, IL 61801, USA
Tel: 2172655473
Email: bohnertlab@life.uluc.edu.
Location/Qualifiers
1. c648
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/db_xref="taxon:4577"
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mM Nacl"
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June 16, 2003, 01:23:01; Search time 1439.61 Seconds (without alignments) 7604.943 Million cell updates/sec
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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		Description		BQ619167 RNOSEQ4E0	BQ619315 RNOSEQ6C0	BQ619318 RNOSEQ6D0	BQ619337 RNOSEQ6E1	BQ619383 RNOSEQ7B0	BQ619390 RNOSEQ7B0
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AW331212 707049E04 BE025302 94502B09 AW28876 707009E07 AY104409 Zea mays AW787732 945002E06 AA979839 MEST2-B7 BG840383 MEST2-B7 AW787314 945002E06 AW787314 945002E06 BE519299 945007B05	ALJOHAS 4-9501010404 ALJOHAS 4-945012012 AW787315 945022012 AW787315 94500200 BE12964 945027005 BE12964 945042F02 BW289056 707005E07 BW501439 PACCODO00 AW745436 WS1_34_B1 BW074540 WS1_34_B1	AW0.7959 WEL-94-BU BES97738 PIL 85-F0 BEG84088 MES712-H1 BF729420 1000077C0 BM318672 PIL 16-C0 AW74763 WSL 74-A0 BES93507 WSL 100_B AW288975 707009E07 AW2284579 WSL 70-G1 BQ283209 WHE3087-E BQ283209 WHE302-G BES93304 WSL 70-G1	nRNA lin mays roots imilar to h yta; Embryc psida; Poal Zea.
AW331212 BE025302 AW288876 AY104409 AM78732 AA979839 BG840383 AW787314 BE519299	A1964458 BEL12987 AW787315 AW787315 A1964534 BEL225008 BW225008 AW745436 AW745400 BES05303 BES044 AW680016 BQ280709 BES99123	AW679569 BE59778 BC64082 BR729420 BR718672 AW747603 AW649804 AW28875 AW28875 BW228209 BQ281558 BE593304	ALIGNMENT 648 bp 1t stressed 2804E05_SK.abb 161 1cophyta; Lil Andropogonea H.J. ress toleran cksen Blology 1s Urbana, IL ( 1cophana, IL ( 1co
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73 72 71 70 69 68 68 67 67 67	66 66 66 66 66 66 66 66 66 66 66 66 66	222223333344452724	BQ619167 RNOSEQ4E05_SK.abl Salmays cDNA clone RNOSE Sequence. BQ619167.1 G1:21621. EST. Eam mays. Lea mays. Clade; Panicoldeae; Ju fasses 1 to 648 Mang, H. and Bohnert) Genomics of plant St. Unpublished (2002). Unpublished (2002). Tel: 217255473 Fel: 2172555473 Fel: 2172555473 Fel: Lohoartlabeli Lohoartla
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1 MAYYQEVDYCSEEVRSVAPA.....INTCTGEVHERRESFLARAN
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US-10-090-035-18

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US-10-090-035-22

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                                                                                                                                                                  392085 seqs, 103240269 residues
                                   - protein search, using sw model
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Sequence 12, Appl
Sequence 129, Appl
Sequence 19, Appl
Sequence 3, Appl 1
Sequence 3, Appl 1
Sequence 1120, Appl
Sequence 317, Appl Sequence 317, Appl Sequence 317, Appl Sequence 317, Appl Sequence 217, Appl Sequence 21, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 201, Appl Sequen
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Sequence 2, Application US/10090035

Patent No. US/20020170089A1

GENERAL INFORMATION:
TITLE OF INVENTION: Notein Actids Encoding Defense Inductble
TITLE OF INVENTION: Proteins and Uses Thereof
TITLE OF INVENTION: Proteins and Uses Thereof
CURRENT APPLICATION NUMBER: US/10/090,035

CURRENT FILING DATE: 2002-02-38

PRIOR APPLICATION NUMBER: 60/272,227

NUMBER OF SED ID NOS: 25

SOFTWARE: FastSED for Windows Version 4.0

LENGTH: 93
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Best Local Similarity 100.0%; Pred. No. 5e-45;
Matches 93; Conservative 0; Mismatches 0; Indels
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| Patent No. US20020170089A1
| GENERAL INFORMATION:
| APPLICART: Simmons, Carl R.
| TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible intile OF INVENTION: Proteins and Uses Thereof
     9 US-09-876-904A-627

10 US-09-824-735-3

10 US-09-813-736-338

12 US-10-052-798-11

10 US-09-925-302-501

10 US-09-933-790-428

9 US-10-108-605-125

9 US-10-108-605-125

9 US-09-932-257A-19

9 US-09-932-257A-19

9 US-09-051-013-3

10 US-09-051-013-3

10 US-09-051-013-9

9 US-09-051-013-9

10 US-09-051-013-9

9 US-10-044-692-317-9

9 US-10-044-692-317-9

9 US-10-044-692-317-9

9 US-10-044-692-317-9

9 US-10-044-692-317-9

9 US-10-044-692-317-9

9 US-09-973-116-9

9 US-09-973-116-9

10 US-09-975-119-201

10 US-09-975-719-201

9 US-09-975-719-199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Zea mays
US-10-090-035-2
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US-10-090-035-4
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1; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 25 SOFTWARE: FastSEQ for Windows Version 4.0
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
                                                                                                                                                                          Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/10090035
Patent No. US20020170089Al
                                                                                                                                                  Query Match
Best Local Similarity 98.9%;
Matches 92; Conservative
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Best Local Similarity 98.93
Matches 93; Conservative
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US-10-090-035-8
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                                                                                                ; ORGANISM: Zea mays US-10-090-035-10
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US-10-090-035-18
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US-10-090-035-8
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Sequence 6, Application US/10090035

Sequence 6, Application US/10090035

Patent No. US20020170089A1

Patent No. US20020170089A1

Patent Information: Carl R.

TITLE OF INVENTION: Mucleic Acids Encoding Defense Inducible

TITLE OF INVENTION: Proteins and Uses Thereof

TITLE OF INVENTION: Proteins and Uses Thereof

TITLE OF INVENTION: Proteins and Uses Thereof

CURRENT APPLICATION WUMBER: US/10/090,035

CURRENT FILING DATE: 2022-228

PRIOR PALICATION WUMBER: 60/272,227

PRIOR FILING DATE: 02/28/2001

NUMBER OF SEC ID NOS: 25

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 93
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Sequence 10. US20020170089A1
Patent NO. US20020170089A1
GENERAL INFORMATION:
APPLICANT: Simmons, Carl R.
APPLICANT: Simmons, Carl R.
TITLE OF INVENTION: Proteins and Uses Thereof
FILE REPERENCE: 35718/242990
CURRENT APPLICATION NUMBER: US/10/090,035
CURRENT FILING DATE: 2002-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 510; DB 9; Length 93; Best Local Similarity 100.0%; Pred. No. 5e-45; Matches 93; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                  100.0%; Score 510; DB 9; : 100.0%; Pred. No. 5e-45; tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 35718/242990
CURRENT APPLICATION NUMBER: US/10/090,035
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 60/272,227
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
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PRIOR FILING DATE: 02/28/2001
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Best Local Similarity 100.0
Matches 93; Conservative
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US-10-090-035-6
                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Zea mays
US-10-090-035-4
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                                                                    1 MAYYQEVDYCSEEVRSVAPAGFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHGHHGG
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Sequence 18, Application US/10090035

Patent No. US20020170089A1

GENERAL INFORMATION:
APPLICANT: Simmons, Carl R.
TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible
TITLE OF INVENTION: Proteins and Uses Thereof
FILE REFERENCE: 35718/242990

CURRENT APPLICATION UNMER: US/10/090,035

CURRENT ELIGATION NUMBER: 60/272,227

PRIOR FILING DATE: 2002-02-28

PRIOR FILING DATE: 02/28/2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 94;
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APPLICANT: Simmons, Carl R.
TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible TITLE OF INVENTION: Proteins and Uses Thereof FILE REFERENCE: 35718/242990
CURRENT APPLICATION NUMBER: 08/10/090,035
CURRENT FILING DATE: 2002-02-28
PRIOR PRILICATION NUMBER: 60/272,227
PRIOR FILING DATE: 02/28/2001
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Length 93;
                                    Indels
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98.9%; Pred. No. 5.9e-44;
iive 0; Mismatches 0;
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pred. No. 1e-44;
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1 MAYYQEVDYCSEEVRSVA-PAGFGRHGGGVQQHVVKEKF-EEVDTVSRAGANHHHHHGHH 58
                                                                        1 MAYYQEVDYCSEEVRSVA-PAGFGRHG-GGVQQHVVKEKF-EEVDTVSRAGANHHHHHGH 57
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TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible
TITLE OF INVENTION: Proteins and Uses Thereof
FILE REPERENCE: 35718/24299
CURRENT APPLICATION NUMBER: US/10/090,035
CURRENT APPLICATION NUMBER: 60/272,237
PRIOR APPLICATION NUMBER: 60/272,227
PRIOR FILING DATE: 02/28/2001
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24
LENGTH: 92
                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Simmons, Carl R.
TITLE OF INVENTION: NUCLEIC Acids Encoding Defense Inducible TITLE OF INVENTION: Proceeding and Uses Thereof FILE REFERENCE: 35718/742990
CURRENT APPLICATION NUMBER: 05/10/090,035
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 60/272,227
PRIOR FILING DATE: 0.208/2001
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 7e-21;
2; Mismatches 12; Indels
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                                                                                                                                   59 G---GHGFVVRETRVEEDINTCTGEVHERRESFLARAN 93
                                                                                                                                                         ; Score 258; DB 9;
; Pred. No. 2.4e-19;
14; Mismatches 13
          Mismatches
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Patent No. US20020170089A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                Sequence 20, Application US/10090035
Patent No. US20020170089A1
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Best Local Similarity 61.6%;
Matches 61; Conservative 13
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58.68;
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US-10-090-035-24
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Best Local Similarity 58.6%
Matches 58; Conservative
          Conservative
        60;
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LENGTH: 92
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          Matches
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                                                                                                                                            1 MAYYQEVDYCSEEVRSVAPAGFGRHGGGVQQHVVKEKFEEVDTVSRAGAN-HHHHHGHHG 59
                                                                                                                                                                    1 MAYYQEVDYCSEEVRSVAP-AGFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHHGHHG
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Patent No. Us20020170089A1
GENERAL INFORMATION:
TTLE OF INVENTION: Nucleic Acids Encoding Defense Inducible
TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible
TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible
TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible
GURRENT APPLICATION NUMBER: US/10/090,035
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 60/272,227
PRIOR APPLICATION NUMBER: 60/272,227
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Mindows Version 4.0
                                                                    Length 94;
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Patent No. US20020170089A1
Patent No. US20020170089A1
PAPENT No. US20020170089A1
PERENAL INFORMATION:
APPLICANT: Simmons, Carl R.
TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible FILE OF INVENTION: Proteins and Uses Thereof FILE REPERENCE: 35718/7442900
CURRENT APPLICATION NUMBER: US/10/090,035
PRIOR APPLICATION NUMBER: 60/272,227
PRIOR FILING DATE: 02/28/2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57.8%; Score 295; DB 9; Length 91 60.6%; Pred. No. 4e-23; tive 14; Mismatches · 19; Indels
                                                                                                           Indels
                                                             Score 499.5; DB 9;
Pred. No. 5.9e-44;
0; Mismatches 0;
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Pred. No. 2.4e-21;
                                                                                                                                                                                                                                60 GHGFVVRETRVEEDINTCTGEVHERRESFLARAN 93
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                                                                                                         0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                             Query Match 97.9%;
Best Local Similarity 98.9%;
Matches 93; Conservative
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61.2%;
; ORGANISM: Triticum aestivum
US-10-090-035-18
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ORGANISM: Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 60.6%
Matches 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
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Sequence 64, Application US/0988615
Patent No. US20020064856A1
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; LOCATION: (1891)
; OTHER INFORMATION: Any amino acid
US-09-888-615-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 -- INTCTGEVHERRESF 88
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33.3%;
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29.9%;
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Best Local Similarity 33...
Local Similarity 33...
Local Similarity 33...
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Best Local Similarity 29.99
Matches 23; Conservative
                                                                                                                                                                                       APPLICANT: PLOWMAN, GREGORY
                                                                                                                                                                                                                                                                                                                                                                                                                                         PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens
US-10-232-563-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
49 A--
                                                                                                              US-09-888-615-64
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LENGTH: 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MAYYQEVDYCSEEVRSVAP-AGFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHHHHHHGHHG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MAYYQEVDYCSEEVRSVAP-----AGFGRHGGGVQOH-----VVKEKFEEVDTVSRAG 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Sharma, Arun
TITLE OF INVENTION: USES THEREOF
FILE OF INVENTION: USES THEREOF
FILE REFERENCE: 10276-072001
CURRENT APPLICATION NUMBER: US/10/232,563
CURRENT FILING APPLE: 2002-08-30
PRIOR APPLICATION NUMBER: US 60/316,453
PRIOR FILING DATE: 2001-08-31
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                     APPLICANT: Simmons, Carl R.
TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible FILE REFERENCE: 35718/242990
CURRENT APPLICATION NUMBER: US/10/090,035
CURRENT FILING DATE: 2002-02-28
PRIOR FILING DATE: 60/22/2,227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 99;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22; Indels
                     HG---GHGFVVRETRVEEDINTCTGEVHERRESFLARAN 93
                                           Score 245; DB 9;
Pred. No. 5.4e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 1.4; 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9; Mismatches
                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION: (1) ...(99)
; OTHER INFORMATION: Xaa - Any Amino Acid
US-10-090-035-14
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                                                                                                                                  US-10-090-035-14
; Sequence 14, Application US/10090035
; Patent No. US20020170089A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/10232563
Publication No. US20030087394A1
GENERAL INFORMATION:
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26.0%;
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Best Local Similarity 58.8%;
Matches 50; Conservative
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Matches 25; Conservative
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; ORGANISM: Mus musculus
US-10-232-563-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Oryza sativa
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                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
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21 GFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHHHHHGHHG-----FVVRETRVEED
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Publication No. US20030087394A1
GENERAL INFORMATION:
APPLICANT: Sharma. Arun
TITLE OF INVENTION: INSULIN RELATED TRANSCRIPTION FACTOR AND
TITLE OF INVENTION: USSS THEREOF
FILE REPERENCE: 10276-072001
CURRENT FILING DATE: 2002-08-30
PRIOR PILING DATE: 2001-08-31
PRIOR FILING DATE: 2001-08-31
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175 ADDMGAGHHHGAННТАНННКАNНННННННGGSG 210
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7; Mismatches
                                                                                                                                                                                          APPLICANT: WHYTE, DAVID
APPLICANT: CAENEPEEL, SEAN
APPLICANT: CAENEPEEL, SEAN
APPLICANT: CHERYDCARK, GLEN
APPLICANT: MANNING, GERARD
APPLICANT: MANNING, GERARD
TITLE OF INVENTION: NOVEL PROTEASES
FILE REFERENCE: 038602/1214
CURRENT APPLICATION NUMBER: US/09/888,615
PRIOR FILING DATE: 2001-06-26
PRIOR FILING DATE: 2000-06-26
NUMBER: OF SEQ. ID NOS: 150
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SOFTWARE: FastSEQ for Windows Version 4.0
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1 MAYYQEVDYCSEEVRSVAP-----AGFGRHGG--GVQQHVVKEKFEEVDTVSRAGA-- 49
                              Ouery Match
Best Local Similarity 25.0%; Pred. No. 2.8;
Matches 24; Conservative 7; Mismatches 29; Indels
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230 QLVSMSVRELNRQLRGF 246
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Sequence 2, Application US/09103840A

Patent No. 6294328

SEMERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILLE REFERENCE: 24366-20007.00

CURRENT APPLICATION NUMBER: US/09/103,840A

CURRENT FILLING DATE: 1998-06-24

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PATENTIN VAF. 2.1
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Matches:
Conservative:
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Indels:
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          US-10-090-035-2 (1-93) x US-09-103-840A-2 (1-4403765)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at
OTHER INFORMATION: represent a,
US-09-103-840A-2
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Best Local Similarity:
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                                                                                              US-10-090-035-2
510
1 MAYYQEVDYCSEEVRSVAPA.....INTCTGEVHERRESFLARAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/ptoTUS_COMB.seq:*
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                                  OM protein – nucleic search, using frame_plus_p2n model
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16.3 4411529 4 US-09-103-840A-1

15.7 2310 3 US-09-305-987A-25

15.7 2310 4 US-09-370-700-25

15.6 195 2 US-08-622-740-9

15.6 195 3 US-08-622-740-9

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15.1 2373 4 US-08-78-275-1

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303 GGAGCIGCACGAGAICGAGGIGGAGACCAICCGGIGGAGACCAICGAGACCACAGIGGI 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 -GlyPheValValArgGluThrArgValGluGluAspIleAsnThrCysThrGlyGluVa 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----GlyGlyGlyValGlnGlnHis-ValVa
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                                                                                                                                                                                 PatentIn Release #1.0, Version #1.25
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Mismatches:
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                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06840
FILING DATE: 19920814
                                                                                                                                CLASSIFICATION:
CLASSIFICATION: AU 1805
PRIOR APPLICATION NUMBER: US 07/746,485
FILING DATE: 16-AUG-1991
ATTORNEY/AGENT INFORMATION:
                      : Floppy disk
IBM PC compatible
YSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                     TELEPHONE: (212) 382-0700
TELEFAX: (212) 382-0888
TELEEX: 236925
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE TYPE: HeLE Cells TISSUE TYPE: Carcinoma CELL TYPE: tumor cells CELL LINE: HeLa
                                                                                                                                                                                                                                                                                                                                                                                             2353 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: NUCLEIC ACID
STRANDEDNESS: double
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CLONE: p14-1 or pYY1
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        READABLE FORM:
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SOFTWARE: PatentI
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ORIGINAL SOURCE
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                          MEDIUM TYPE:
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PCT-US92-06840-1
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                                                                                         3228651 CCGACTGCTCAGCCTGTTCGAACAGCTGCGAGAGCAGCAGCAGCATCATCATCATCACCCA 3228592
                             3228711 TCCATCGCCGTTCTACATCATGGACGAGGTGGAGGCCGCCCTCGACGTGAACCTGCG 3228652
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SerValAlaProAlaGlyPheGlyArgHisGlyGlyGlyValGlnGlnHisValValLys 35
                                                                  54
                                                                                                                                                     36 GluLysPheGluGluValAspThrValSerArgAlaGlyAlaAsnHisHisHisHis---
                                                                                                                                                                                                                                                                                                   APPLICANT: WHITE. OWEN R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, Oldn C.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 2436-20007.00
CURRENT RAPPLICATION UNMARE: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---HisGlyHisHisGlyGlyHisGlyPheValNalArgGluThrArgValGlu 71
                                                                                                                                  55 ---HisGlyHisHisGlyGlyHisGlyPheValValArgGluThrArgValGlu 71
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APPLICANT: Seto, Edward
APPLICANT: Seto, Edward
TITLE OF INVENTION: YY1 TRANSCRIPTION FACTOR AND METHODS OF
TITLE OF INVENTION: ISOLATING SAME
TITLE OF INVENTION: ISOLATING SAME
OUTBRER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Ostrolenk, Faber, Gerb & Soffen STREET: 1180 Avenue of the Americas - 7th Floor CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 4411529
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 1, Application PC/TUS9206840; GENERAL INFORMATION:
                                                                                                                                                                                                                                      Sequence 1, Application US/09103840A
Patent No. 6294328
                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.22e+04
83.00
46.55%
36.21%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: H37Rv
US-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 2
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Best Local Similarity:
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                                                                                                                                                                                                                           US-09-103-840A-1/C
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	Oy 27 GlyGlyValGlnGlnHisValValLysGluLysPheGluGluValAspThrValSerArg 46		Db 312 GGACATCAGGCCGCCAACCAGTTCGCGGTCGCAGATGCCGCAAA 262	Qy 76 ThrCysThrGlyGluValHisGluArgArgGlu 86              ::     :: Db 261 CTTCAGCCGGGGTTGTCCGCGACCGCCAG 229		; Sequence 25, Application US/09370700 ; Patent No. 6274350 ; GENERAL INFORMATION:	ichard H	APPLICANT: Madduri, Krishnamurthy APPLICANT: Treadway, Patti J		; FILE OF INVENTION: BIOSYNCHETIC Genes For Spinosyn Insecticide ; FILE REFERENCE: 50489 DIVI ; CURRENT APPLICATION NIMBED: 15,000,200	CURRENT FILING TOWN NUMBER: US/US/3/U,/UU  EARLIER APPLICATION NIMBS-08-09	: EARLIER FILING DATE: 1998-03-09	; SOFTWARE: Patentin Ver. 2.0 ; SEQ ID NO 25	TYPE: DNA  CREANISM: SACCHBATOMOLIVEROUS CONTRACTOR		; LCCATION: (88)(1077) ; FEATURE: . NAME YERY, CRC	; NCATION: (1165)(1992) US-09-370-700-25	1.24 Length:	Score: 80.00 Matches: 27 Percent Similarity: 41.76% Conservative: 11 Best Local Similarity: 29.67% Mismatches: 35	15.69% Indels: 4 Gaps:	-10-080-01-	Ty AtaspryrCysSerGluGluValargSerValalasproalaGlyPheGlyArgH1sGly 26	SerArg	426	47		
Db 483 GCCCATGATCGCTCTGCAGCCGCTGGTCACCGACGACCCGACCCAGGT 530	<pre>Qy 81 lHisGluArgArgGluSerPheLeualaarg 91</pre>	RESULT 4 US-09-036-987A-25/C ; Sequence 25, Application US/09036987A ; Fattent No. 614353564	APPLICANT: Broughton, Mary C. APPLICANT: Crawford Mary C.	APPLICANT: Madduri, Krishnamurthy APPLICANT: Merlo, Donald J. ; APPLICANT: Treadway, Patti J.	Turner, Jan R. Waldron, Clive NVENTION: Ricevonthetic Const.	TITLE OF INVENTION: Production  WUMBER OF SEQUENCES: 39  CORRESPONDENCE ADDRESS:	ADDRESSEE: Dow AgroSciences LLC Patent Department STREET: 9310 Zionsville Road TTV.		COMPUTER READBLE FORM:	COMPUTER: FIOPPY GISK COMPUTER: IS TO COMPATING COMPUTER: DELEGEMENT OF THE COMPATING	SOFTWARE: Patentin Release #1.0, Version #1.30	APPLICATION NUMBER: US/09/036,987A FILING DATE: 09-MAR-1998	CLASSIFICATION: 435 TTORNEY/ACENT INFORMATION:	NAME: Stuart, Donald R REGISTRATION NUMBER: 28,479 REFERENCE/DOCKET NIMBER: 60 600	INFORMATIC 7)337-4816	TELEFAX: (317)337-4847 ; INFORMATION FOR SEQ ID NO: 25: SPOITENCE CHARACTERIOR 25:	CONCRETE CHARACTERS:  LENGTH: 2310 base pairs  TYPE: nucleic acid	STRANDEDNESS: double TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)	FEATURE: NAME/KEY: CDS : LOSTION: 881077	EY:	n.	1.24 Length: 80.00 Matches:	Fercent Similarity: 41.76% Conservative: 11 Best Local Similarity: 29.67% Mismatches: 35 Query Match: 15.69% Todal 20.000	3 Caps:	-10-090-035-	OY 7 ValAspTyrCysSerGluGluValArgSerValAlaeproAlaGlyPheGlyArgHisGly 26 Hilli Db 480 GTAGACTECTECTECTECTECTECTECTECTECTECTECTECTEC	427

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GENERAL INFORMATION:
APPLICANT: Lundquist, Ronald C.
APPLICANT: Walters, David A.
APPLICANT: Walters, Julie A.
APPLICANT: Kirihara, Julie A.
TITLE OF INVENTION: Methods and Compositions for the
TITLE OF INVENTION: Production of Stably Transformed, Fertile Monocot Plants
                                                                                              APPLICANT: Kirihara, Julie A. TITLE OF INVENTION: Methods and Compositions for the TITLE OF INVENTION: Methods and Compositions for the TITLE OF INVENTION: Production of Stably Transformed, Fertile Monocot Plants TITLE OF INVENTION: and Cells Thereof NUMBER OF SEQUENCES: 22 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 SerValAlaProAlaGlyPheGlyArgHisGlyGlyGlyValGlnGlnHisValValLys 35
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BATCOMPACED
COMPUTER: OF COMPACED
COMPUTER: OF COMPACED
COMPUTER: OF COMPACED
CONFREMT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,689
FILING DATE: 15-MA-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: WOSSENEY, WAITEN D.
REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 30,440
                                                                                                                                                                                                                                 ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth,
STREET: 3500 IDS Center
CITY: Minneapolis
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Indels:
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Matches:
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9, Application US/08440689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION
TELEPHONE: 612-339-0331
TELEFAX: 612-339-3061
                                                                        APPLICANT: Lundquist, Ronald
APPLICANT: Walters, David A.
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48.98%
46.94%
15.59%
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
                                 Patent No. 6025545
GENERAL INFORMATION:
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US-09-122-399-9/c
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STATE: MN
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APPLICANT: Walters, David A.
APPLICANT: Walters, David A.
TITLE OF INVENTION: Methods and Compositions for the
TITLE OF INVENTION: Production of Stably Transformed, Fertile Monocot Plants
TITLE OF INVENTION: and Cells Thereof
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
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                  312 GGACATCAGGCCGCCAACCAGTTCGCGGTCGCAGATGTCGCCGCAGACGAA-
                                                                                                                                                                                                                                                                                                                                                                                                                      SEE: Schwegman, Lundberg, Woessner & Kluth, P.A.
: 3500 IDS Center
Minneapolis
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APPLICATION NUMBER: US/08/622,740
FILING DATE: 27-MARCH-1996
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative:
Mismatches:
Indels:
                                                                                          111 | | | | :::||||||:::
261 CTTCAGCCGGGGTTGTCCGCGACCGGCGCAG 229
                                                                 76 ThrCysThrGlyGluValHisGluArgArgGlu 86
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Matches:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Woessner, Warren D.
REGISTRATION NUMBER: 30,440
REFRENCE/DOCKER NUMBER: 950.(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-3061
TELEFAX: 612-339-3061
                                                                                                                                                                                         Sequence 9, Application US/08622740 Patent No. 5990390 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
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48.98%
46.94%
15.59%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 195 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
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CITY: Minne
STATE: MN
COUNTRY: US
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US-08-440-689-9/c
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                                                                                                                                                       RESULT 6
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1858 CAGAATGCATTGCATCATCACCATGGTAACAGTTCCCATCATCACCACCACCACCACCAC 1917
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|1738 AGTCCCCAGGTCAGTCAGTTTCCTGCTCTTGGTTGGTCAGGCACTGAAGCTCCT | 1797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1798 ACACAGGICACTGITGAAACICCATCCTGITCAAGAAACAACCTITCATGIAGCCCCTCAA 1857
                                                                                                                                                                                                                                                                                                                                                                                                                                                             28 ------GlyValGlnGlnH1sValValLysGluLysPheGluGluValAspThrVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45 Serargala--------GlyalaAsnHisHisHisHisHisGly
                                                                                                                                                                                                                                                                                                                                                                                 11 SerGluGluValArgSerValAlaProAlaGlyPheGlyArgH18GlyGly-----
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22
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26
14
26
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ZIP: 94111
COMPUTER READABLE FORM:
MEDIUW TYPE: FLOPPY disk
COMPUTER: IBM PC COMPATIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEMITIN Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/677,862
FLING DATE:
FLING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: SONG, HO YEONG

TITLE OF INVENTION: TRAF2-ASSOCIATED Kinase

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Flehr, Hobbach, Test, Albritton & H
STREET: 4 Embarcadero Center, 34th floor

CITY: San Francisco
                                                                                                                                                                                                                                                         Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                             US-10-090-035-2 (1-93) x US-08-789-275-1 (1-2373)
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                                                                                                                                                                                                                                                                                                                   Gaps:
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Patent No. 5874230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Brezner, David J
REGISTRATION NUMBER: 24,774
REFRENCE/DOCKET NUMBER: T96-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415,398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57 HisHisGlyGlyHisGly 62
                     CURRENT FILING DATE: 1997-01-28 UNDMER OF SEQ ID NOS: 6 SEQ ID NO 1 LENGTH: 2373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3218 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear
                                                                                                                                                                                                                 3.05
77.00
39.39%
33.33%
15.10%
                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                         Best Local Similarity:
                                                                                                                                                                                                                                                   Percent Similarity
                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                         US-08-789-275-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 GluLysPheGluGluValAspThrValSerArgAlaGlyAlaAsnHisHisHisHis 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111 GAGCCCCTGGAACGGAGCGACGCGGTGGCCGACGAGGC------CATCATCAC 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Palleja, Estivill Xavier
APPLICANT: Palleja, Estivill Xavier
APPLICANT: Pitchard, Melande.
APPLICANT: Vilaro, Jordi Guimera
TITLE OF INVENTION: Human Gene Sequence of the Down Syndrome Critical
TITLE OF INVENTION: Region of Human Chromosome 21, Coding for A Serine-
TITLE OF INVENTION: Threonine Protein Kinase (MNB), Expressed in the
TITLE OF INVENTION: Neuronal Regions Affected in Down Syndrome
FILE REFERENCE: U 011114-4
CURRENT APPLICATION NUMBER: US/08/789,275A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     195
23
1
13
12
                       NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg & Woessner, P.A.
STREET: 3500 IDS Center
CITY: Minneapolis
                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/09/122,399
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: WOSSIGE, WAITEN D.
REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 950.13US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-031
TELEPHONE: 612-339-061
INFORMATION FOR SEC ID NO: 9:
SEQUENCE CHARACTERISTICS:
FITLE OF INVENTION: and Cells Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/112,245
FILING DATE: 25-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08789275A Patent No. 6251664
                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 195 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79.50
48.98%
46.94%
15.59%
                                                                                                                                                       ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity;
Query Match:
                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                           FILING DATE:
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                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-122-399-9
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US-08-789-275-1
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                                                                                                                                                                                                                                                                                                      45 Serargala-------GlyalaasnHisHisHisHisGly 56
                                                                                                                                                                                                                                 28 ------GlyValGlnGlnHisValValLySGluLySPheGluGluValAspThrVal 44
                                                                                                                                                                11 SerGluGluValArgSerValAlaProAlaGlyPheGlyArgH1sGlyGly-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: SONG, Ho Yeong
APPLICANT: ROTHE, Mike
TITLE OF INVENTION: TRAF2-Associated Kinase
TITLE OF INVENTION: TRAF2-Associated Kinase
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS: 2
ADDRESSE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: 4 Embarcadero Center, 34th floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3218
22
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22
4
26
14
2
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APPLICATION NUMBER: US/09/434,065
                           Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                  US-10-090-035-2 (1-93) x US-09-252-571-1 (1-3218)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Brezner, David J
REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: T96-005/A63613
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415 781-1989
TELEFRAX: 415 398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
             Length:
                                                                                                    Gaps:
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APPLICATION NUMBER: 08/677,862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09434065
Patent No. 6107074
                                                                                                                                                                                                                                                                                                                                                                                                                    1963 CATCACCACCACCATGGA 1980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 415 398-3249
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    57 HisHisGlyGlyHisGly
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                                                39.39%
33.33%
15.10%
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                                       Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Pred. No.:
Score:
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Alignment Scores:
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US-09-434-065-1
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                      Pred. No.:
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                                                                                                                                                                                                                                 11 SerGluGluValArgSerValAlaProAlaGlyPheGlyArgHisGlyGly-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ROTHE, Mike
APPLICANT: ROTHE, Mike
TITLE OF INVENTION: TRAF2-Associated Kinase
TUTHE OF SEQUENCES: 2
CORRESPONDENCES: ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: 4 Embarcadero Center, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/252,571
                                                                                                             Conservative:
Mismatches:
Indels:
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                                                                              Length:
Matches:
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APPLICATION NUMBER: 08/677,862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BREZIER, DAYAJ J
REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: T96-(
TELECOMMUNICATION INFORMATION:
TELEFONE: 415 781-1989
TELEFAX: 415 398-3249
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1963 CATCACCACCATGGA 1980
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; Sequence 1, Application US/09252571
; Patent No. 5981250
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                                                                                4.58
77.00
39.39%
33.33%
15.10%
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STRANDEDNESS: double
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     San Francisco
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                                                                                                          Percent Similarity:
Best Local Similarity:
Query Match:
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US-09-252-571-1
           ; MOLECULE TYPE:
US-08-677-862-1
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                                                                 Alignment Scores:
Pred. No.:
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Percent Similarity: 45.61% Conservative: 8 Best Local Similarity: 31.88% Mismatches: 25 Query Match: 14.90% Indels: 6 DB: 4 Gaps: 1	103)	Oy 11 SerGluGluValArgSerValAlaProAlaGlyPheGlyArgHisGlyGlyGlyValGl	31	463 GAGGAGTGGGCCCGCCGCCGTGGTGTCCCGCCGTGATCGCCGCGGCCC	QY 45 SerargalaGlyalaasnHisHisHisHisHisGlyHisHisGlyGlyHisHis 61	SULT 14 -09-329-	; Sequence 6, Application US/09329234A ; Patent No. 6331416 ; GENERAL INFORMATION:	APPLICANT: Shani, Ziv	TILLE OF INVENTION: PROCESS OF EXPRESSING AND ISOLATING RECOMBINANT PR. TILLE OF INVENTION: PROTEIN PRODUCTS FROM PLANTS, PLANT DERIVED TISSU	CURRENT APPLICATION NUMBER: US/09/329,234A	NUMBER OF SEQ ID NOS: 8  .; SOFTWHEE Patentin version 3.1 : SEO TO NO 6	; LENUTH: 1305	) ORGANISM: Artificial sequence	; OTHER INFORMATION: Construct containing Protein L, fused to CBDcex sec US-09-329-234A-6	ent Scores: 3.27 Length:	74.00 Matches: 40.91% Conservative:	t Local Similarity: 36.36% ry Match:	Gaps: 1 US-10-090-035-2 (1-93) x US-09-329-234A-6 (1-1305)	Oy 19 ProAlaGlyPheClyArgHisGlvGlvGlvGlvGlvGl	Db 1173 CCGCGGCGCACCGCGCAGTTCGGCTTCAACGCCTCGACACGGGCACCAACGCCCGG	Oy 35 LysGluLysPheGluGluValAspThrValSerArgAlaGlyAlaAsnHisHisHisHis	Db 1233 CGACGGGGTTCTCGCTCAACGCCCTGCACGGTCGGCGTCGGCGTCGACCACCACCACCACCACCACCACCACCACCACCACCAC	Qy 55 H1sG1yH1sH1s 58	Db 1293 CACCACCAC 1304	RESULT 15 US-08-240-783B-1/C	; Sequence 1, Application US/08240783B ; Patent No. S75548 ; GEMERAL INFORMATION:	; APPLICANT: Smith, Kelli ; APPLICANT: Borden, Laurence A.
39.39% Conservative: 4 33.33% Mismatches: 26 15.10% Indels: 14 3 Gaps: 2	(1-93) x US-09-434-065-1 (1-3218)	SerGluGluValArgSerValalaProalaGlyPheGlyArgHisGlyGly 27     :::	190	HisHisHisHisGlv	SACCATGGTAACAGTTCCCATCACCATCACCACCACCACCACCACCACCACCAC	57 H18H1sGlyGlyH1sGly 62 		Sequence 1, Application US/09086010 Patent NO. 6774338	.wk.nt. nroVnATION: APPLICANT: Glimcher, Laurie H. et al. IITLE OF INVENTION: Human c-Naf Compositions and		CORRESPONDENCE ADDRESS: ADDRESSEE: LAHIVE & COCKFIELD, LLP STREET. 38 C+++- C+-+	CITY: Boston Street STATE: Massenhaetts	YY: USA 02109	COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk	COMPUTER: IBM PC compatible OPPRATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #11.0. Vereion #1.26	ATION DATA: NUMBER: US/09/086,010	FILING DATE:	FALOR AFFLICATION NUMBER: 09/030,579 FILING DATE: 2-FEB-1998	ATTORNEY/AGENT INFORMATION: NAME: Kara, Catherine J.	REGISTRATION NUMBER: 41,106 PROFERENCE/DOCKET NUMBER: HUI-027CP	TELEPHONE: (617)27-7400	INFORMATION FOR SEQ ID: SEQUENCE CHARACTERISTERS	1200 base pairs	STRANDEDMESS: single	MOLECULE TYPE: CDNA FEATURE:	CDS 11203	

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PROTEINS AND R
        CGGC 462
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Scag 522
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CAC 1292
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1Gln 30
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133 GATGTACGT-----GGACACCACCATCATACCATAGCCCACGCCTTTGAACATGGGGCT 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44 ValSerArgAlaGlyAlaAsnHisHisHisHisHisGlyHisGlyGlyHisGlyPhe 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27 ------GlyGlyValGlnGlnHisValValLysGluLysPheGluGluValAspThr 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 CysSerGluGluValArgSerValAlaProAlaGlyPheGlyArgHisGly-----
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1795/39875-A-PCT-US
REFERENCE/DOCKET NUMBER: 1795/39875-A-PCT-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEPHONE: (212) 391-0525
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-090-035-2 (1-93) x US-08-240-783B-1 (1-2121)
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ORIGINAL SOURCE:
ORGANISM: RAT GLYCINE TRANSPORTER
CELL TYPE: MAMMALIAN
CELL LINE: COS7
IMMEDIATE SOURCE:
CLONE: rB20a
FEATURE:
                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                         COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240,783B
                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 800
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; OTHER INFORMATION:
US-08-240-783B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: both
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown
                                                                                                                           New York
: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                          New York
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                                                                                                                                                          ZIP: 10036
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Pred. No.:
                                                                                                       CITY: Nev
STATE: Ne
COUNTRY:
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Search completed: June 16, 2003, 12:40:53
Job time : 1414 secs
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DNA ENCODING A GLYCINE TRANSPORTER AND USES THEREOF
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Sequence 17, Appl Sequence 7, Appl Sequence 19, Appl Sequence 19, Appl Sequence 19, Appl Sequence 13, Appl Sequence 113, Appl Sequence 114, Appl Sequence 17, Appl Sequence 17, Appl Sequence 14, Appl Sequence 14, Appl Sequence 14, Appl Sequence 14, Appl Sequence 13, Appl Sequence 17, Appl Sequence 173, Appl Sequence 174, Appl Sequenc
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Sequence 7, Appli
Sequence 15, Appl
Sequence 457, App
Sequence 6480, Ap
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Fatent No. US20020170089A1
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible
TITLE OF INVENTION: Proteins and Uses Thereof
TITLE OF INVENTION: Proteins and Uses Thereof
CURRENT APPLICATION NUMBER: US/10/090,035
FILE REFERENCE: 35718/242990
CURRENT FILING DATE: 2002-02-28
FRIOR APPLICATION NUMBER: 60/272,227
FRIOR APPLICATION NUMBER: 60/272,227
NUMBER OF SEQ ID NOS: 25
SOFWWARE: FastSEQ for Windows Version 4.0
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9 US-10-090-035-13
10 US-09-923-876-278B
10 US-09-923-876-278B
10 US-09-938-842A-185B
10 US-09-938-842A-185B
10 US-09-938-842A-185B
10 US-09-938-846-13254
10 US-09-938-86-13254
10 US-09-988-615-5
10 US-09-988-615-5
10 US-09-900-237-5
9 US-10-232-563-4
10 US-09-969-347-216
9 US-10-232-563-5
10 US-09-969-347-216
9 US-09-989-343-343
10 US-09-973-973-343
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12 US-10-153-668-95
12 US-09-988-10-163-99
9 US-10-153-668-95
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Matches:
Conservative:
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US-09-918-995-6480
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US-10-090-035-3
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ORGANISM: Zea mays
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US-10-090-035-3
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"MODEL-frame+_p2n.model -DEV-x1h
-0-Ycgn2_1/05F02_pool_/US10090035/runat_06062003_105507_11116/app_query.fasta_1.526
-0-Ycgn2_1/05F02_pool_/US10090035/runat_06062003_105507_11116/app_query.fasta_1.526
-10B=Published_Applications_N -0FMT=fastap -SUFFIX-rnpb -MINMATCH-0.1
-TRAMS-humand40.cdl -LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MAX-100
-TRAMS-Numand40.cdl -LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MAX-100
-MAXLEN-2000000000 -USER-US10090035_GCGN_1_1_176_grunat_06052003_105507
-NCPU-6 -ICPU-3 -NO_MMAP -LARGEQUERY -NGE_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS=1 -XGAPOP=10 -XGAPEXT-0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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1077.357 Million cell updates/sec
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Sequence 5, P
Sequence 1, P
Sequence 9, P
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1. /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2. /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3. /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
4. /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
5. /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6. /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
7. /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8. /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
9. /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
10. /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
11. /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
12. /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
13. /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
13. /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
14. /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
                                                                                                                                                                                       June 16, 2003, 11:41:43 ; Search time 125 Seconds
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                    nucleic search, using frame_plus_p2n model
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US-10-090-035-5
US-10-090-035-1
US-10-090-035-9
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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; LOCATION: (89)...(367)
US-10-090-035-1
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Best Local Similarity:
Query Match:
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                                                                                                                                                  TITLE OF INVENTION: CLALL N.
TITLE OF INVENTION: Proteins and Uses Thereof
FILE REFERENCE: 35718/242990
CURRENT APPLICATION NUMBER: US/10/090,035
CURRENT APPLICATION NUMBER: 60/272,227
PRIOR FILING DATE: 02/28/2001
PRIOR FILING DATE: 02/28/2001
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 577
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Matches:
Conservative:
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                                 US-10-090-035-2 (1-93) x US-10-090-035-3 (1-574)
                                                                                                                                                                                                                                         Sequence 5, Application US/10090035
Patent No. US20020170089A1
GENERAL INFORMATION:
APPLICANT: Simmons, Carl R.
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510.00
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 100.00%
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NAME/KEY: CDS

LOCATION: (99)...(377)

US-10-090-035-5
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Best Local Similarity:
Query Match:
DB:
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   Similarity:
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Sequence 1. Application US/10090035
; Sequence 1. Application US/10090035
; Patent No. US20020170089A1
; GENERAL INFORMATION:
    APPLICANT SIMMONS Carl R.
    TITLE OF INVENTION: NUCLEAC Acids Encoding Defense Inducible
    TITLE OF INVENTION: Proteins and Uses Thereof
    TITLE OF INVENTION: Proteins and Uses Thereof
    TITLE OF INVENTION: Proteins and Uses Thereof
    TITLE OF INVENTION: PROTEINS 2092-02-28
    CURRENT APPLICATION NUMBER: 60/272,227
    PRIOR PILING DATE: 205-22-28
    NUMBER OF SEQ ID NOS: 25
    SEQ ID NOS: 25
    SEQ ID NO 1
    SEQ ID NO 1
    LENGTH: 676
    MANDER: AND 1
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GENERAL INFORMATION:
GENERAL INFORMATION:
Carl R.
APPLICANT: Simmons, Carl R.
TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible
TITLE OF INVENTION: Proteins and Uses Thereof
FILE REFERENCE: 35718/242990
CURRENT APPLICATION NUMBER: US/10/090,035
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 60/272,227
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Matches:
Conservative:
Mismatches:
Indels:
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; Patent No. US20020170089A1
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21 GlyPheGlyArgHisGlyGlyGlyValGlnGlnHisValValValLysGluLysPheGluGlu 40
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                                                                                                                                                                    MetAlaTyrTyrGlnGluValAspTyrCysSerGluGluValArgSerValAlaProAla
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Fatent No. US20020170089A1
GENERAL INFORMATION:
APPLICANT: SIMMONS, Carl R.
ITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible
FITLE OF INVENTION: Proteins and Uses Thereof
FITLE OF INVENTION: Proteins and Uses Thereof
CURRENT APPLICATION NUMBER: US/10/090,035
CURRENT APPLICATION NUMBER: 00/272,227
FRIOR APPLICATION NUMBER: 60/272,227
FRIOR APPLICATION NUMBER: 60/272,227
FRIOR SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                    US-10-090-035-2 (1-93) x US-10-090-035-17 (1-524)
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; LOCATION: (99)...(380)
US-10-090-035-7
             Similarity:
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Best Local Similarity:
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ORGANISM: Zea mays
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Query Match:
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; Patent No. US20020170089A1
; General Information
; Tatent No. US20020170089A1
; GENERAL INFORMATION:
; TILLE OF INVENTION: Proteins and Uses Thereof
; TILLE OF INVENTION: Proteins and Uses Thereof
; FILE REFERENCE: 357182A2990
; CURRENT APPLICATION NUMBER: US/10/090,035
; CURRENT APPLICATION NUMBER: 05/12/229
; PRIOR RILING DATE: 2002-02-28
; PRIOR FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
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93
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Matches:
Conservative:
Mismatches:
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Matches:
Conservative:
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PRIOR FILING DATE: 02/28/2001
NUMBER OF SEQ ID NOS: 25
SEQTYARE: PastSEQ for Windows Version 4.0
SEQ ID NO 9
LENGTH: 529
                                                                                                                                                                                                            Gaps:
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GRANISM: Triticum aestivum
FRATURE:
NAME/KEY: CDS

LOCATION: (57)...(338)
NAME/KEY: misc_feature
LOCATION: (1)...(524)
COTHER INFORMATION: n = A,T,C or G
                                                                                                                                                2.93e-58
507.00
100.00%
98.92%
99.41%
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499.50
98.94%
                                                                                       ) NAME/KEY: CDS
) LOCATION: (53)...(331)
US-10-090-035-9
                                                        TYPE: DNA
ORGANISM: Zea mays
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Best Local Similarity:
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Pred. No.:
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Alignment Scores:
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                                                                                                                          Sequence 15, Application US/10090035
; Sequence 15, Application US/10090035
; Patent No. US20020170089A1
; GENERAL INFORMATION:
    TITLE OF INVENTION:
    TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible
    TITLE OF INVENTION: Proteins and Uses Thereof
    TITLE OF INVENTION: NUMBER: US/10/090,035
    CURRENT FILING DATE: 2002-02-28
    PRIOR APPLICATION NUMBER: 60/272,227
    PRIOR APPLICATION NUMBER: 60/272,227
    NUMBER OF SEQ ID NOS: 25
    SOFTWARE: FastSEQ for Windows Version 4.0
    SEQ ID NO 15
    LENGTH: 591
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Sequence 21, Application US/10090035
Patent No. US20020170089A1
GENERAL INFORMATION:
APPLICANT: Simmons, Carl R.
TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible
TITLE OF INVENTION: Proteins and Uses Thereof
FILE REFERENCE: 35718/242990
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Mismatches:
Indels:
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Matches:
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295.00
75.53%
60.64%
57.84%
                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Oryza sativa
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Query Match:
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165 CAGGAGTTCGACACCTCCGGCCGC-----CGCCACGGTCACCACGGTCACCAC 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39 GluGluValAspThrValSerArgAlaGlyAlaAsnHisHisHisHisHisGlyHisHis
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CURRENT APPLICATION NUMBER: US/10/090,035
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 60/272,227
PRIOR FILING DATE: 2002-28/2001
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
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60
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Mismatches:
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                                                                                                                                                                                                                                                                                                       Length:
Matches:
CURRENT APPLICATION NUMBER: US/10/090,035
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 60/272,227
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: 436
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Patent No. US20020170089A1
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277.50
73.478
61.228
54.41%
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                                                                                                                                                           TYPE: DNA ORGANISM: Triticum aestivum
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LOCATION: (46)...(321)
NAME/KEY: misc_feature
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LOCATION: (54)...(326)

US-10-090-035-21
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OTHER INFORMATION: n
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Best Local Similarity:
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58 HisGly------GlyHisGlyPheValValArgGluThrArgValGluGluAsplle 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29
                                                                                                                    39 ---GluGluValAspThrValSerArgAlaGlyAlaAsnH1sH1sH1sH1sH1sGlyH1s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40 GluValAspThrValSerArgAlaGlyAlaAsnHisHisHisHisHisGlyHisHisGly
                                                                                                                                                                             US-10-035-13

Sequence 13, Application US/10090035

Fatent No. US20020170089A1

SERVERAL INFORMATION:

FAPLICANT: Simonos, Carl R.

TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible

TITLE OF INVENTION: Proteins and Uses Thereof

TITLE OF INVENTION: Proteins and Uses Thereof

TITLE OF INVENTION: UNMBER: 02/10/090,035

CURRENT FILING DATE: 2002-02-28

FRIOR PAPLICATION NUMBER: 60/272,227

FRIOR PAPLICATION NUMBER: 60/272,227

NUMBER OF SEQ ID NOS: 25

SOFTWARE FARSEO for Windows Version 4.0
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1748
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Matches:
Conservative:
Mismatches:
Indels:
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US-09-923-876-2788
; Sequence 2788, Application US/09923876
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251.00
70.59%
60.00%
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NAME/KEY: CDS

LOCATION: (52)...(348)

NAME/KEY: misc_feature

LOCATION: (1)...(348)

OTHER INFORMATION: n = A

US-10-090-035-13
                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Oryza sativa
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Best Local Similarity:
Query Match:
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LENGTH: 348
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Sequence 23, Application US/10090035
Patent No. US2002017008941
Settle No. US2002017008941
TITE OF INVENTION:
TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible TITLE OF INVENTION: Proteins and Uses Thereof
FILE REFERENCE: 35718/242990
CURRENT APPLICATION NUMBER: US/10/090,035
CURRENT APPLICATION NUMBER: 60/272,227
PRIOR APPLICATION NUMBER: 60/272,227
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 584
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58
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   Length:
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Matches:
Conservative:
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| LOCATION: (46)...(321)
| NAME/KET: misc_feature
| LOCATION: (1)...(584)
| OTHER INFORMATION: n = A,T,C or us-10-090-035-23
3.13e-25
258.00
72.73%
58.59%
50.59%
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258.00
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                   Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
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Pred. No.:
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70 ValGluGluAspIleAsnThrCysThrGlyGlu 80
                  Mismatches:
Indels:
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US-09-938-842A-1858
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50.70%
33.80%
18.14%
   50.70%
33.80%
18.14%
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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US-09-938-842A-1858
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             ; Patent No. US20020013958al
; GENERAL INCPRARATION:
APPLICANT: Lalgudi, Raghmath V.
APPLICANT: Lalgudi, Radigaki, Laura Y. (Ito)
APPLICANT: Sherman, Braday K.
TILLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
FILE REFERENCE: PL-0012-1 CON
CURRENT APPLICATION NUMBER: US/09/923,876
CURRENT FILING DATE: 1999-04-21
PRIOR PLILOG DATE: 1999-04-21
PRIOR PLICATION NUMBER: 60/085,331
PRIOR FILING DATE: 1998-05-05
NUMBER OF SEQ ID NOS: 6332
SOFTWARE: PERL PROGRAM
SEQ ID NO 2788
SEQ ID NO 2788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GlyPheGlyArgHisGlyGlyGlyValGlnGlnHisValValLysGluLysPheGluGlu 40
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                                                                                                                                                                                                                                                                                                                             | NAME/KEY: misc_feature
| OTHER INFORMATION: Incyte ID No. US20020013958A1 700161180H1
| NAME/KEY: unsure
| LOCATION: 125-146, 202
| OTHER INFORMATION: a, t, c, g, or other
| US-09-923-876-2788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: GTACCh, Jrn
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
CURRENT APPLICATION UNBER: US/09/924,035A
CURRENT FILING DATE: 2000-08-11
FRIOR PAPLICATION NUMBER: US 60/148,784
PRIOR FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 900
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 17
LENGTH: 328
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Arabidopsis thaliana
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80.00%
41.76%
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Zea mays
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Pred. No.:
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Sequence 1856, Application US/09938842A

Sequence 1856, Application US/09938842A

Sequence 1856, Application US/09938842A

GENERAL INFORMATION:
APPLICANT: Harper, Jeff

APPLICANT: Wang, Xun
APPLICANT: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
TITLE OF INVENTION UNMBER: US 60/227,866
PRIOR FILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379

SEQ ID NO 1858

LENGTH: 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       295 GGAGGAGGAGTGAACGGTGGTGGAGATATGTCGGCGGCGTATATAAGGAGAAAAGCGGCG 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53 HisHisHisGlyHis---HisGlyGlyHisGlyPheValValArgGluThr----Arg 69
                                                                                                                                                                                                                                                                                                                                                                            208 CATCATCATCAACATCAACGTGGTAATCATGATTACGTAGATAATCATAGTGATTATCGT 149
                                                                                                                                                                                                                                                                      ----AsnHisHis 52
                                                                                                                                                 GlyPheGlyArgHisGlyGly---ValGlnGlnHisValValLysGluLysPheGlu 39
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||| ||| ||| ||| ||| ||||
                                                                                                                                                                             53 HisHisGlyHis---HisGlyGlyHisGlyPheValValArgGluThr----Arg
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           70 ValGluGluAspIleAsnThrCysThrGlyGlu 80
                                                                                                           US-10-090-035-2 (1-93) x US-09-924-035A-17 (1-328)
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11111111111111111 | 111111 | 11111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 |
                                                                                                                                                                                                             Sequence 417. Application US/09728445

Patent No. US20020102543A1

GENERAL INFORMATION:
APPLICANT: Friedrich, Glenn
APPLICANT: Sambrowicz, Brian
APPLICANTON: No. US20020102543A1e1 Mutated Mammalian Cells and
TITLE OF INVENTION: Animals
FILE REFERENCE: LEX-0102-USA
CURRENT PLICATION NUMBER: US 60/168,358
FRIOR FILING DATE: 2000-11-30
FRIOR FILING DATE: 1999-12-01
NUMBER OF SEQ ID NOS: 891
SEQ ID NO 817
LENGTH: 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50 AsnHisHisHisHisHisHisGlyHisHisGlyPheValValArgGluThrArg 69
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Indels:
Gaps:
475 ATTAATGATGATGATGATGATGAAAA 507
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Job time : 132 secs
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LOCATION: (1)...(546)
GTHER INFORMATION: n = A,T,C or G
US-09-728-445-817
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ORGANISM: Mus musculus
FEATURE:
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US-09-728-445-817
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

June 6, 2003, 12:48:33 ; Search time 25 Seconds (without alignments) 357.620 Million cell updates/sec Run on:

US-10-090-035-2 510 1 MAYYQEVDYCSEEVRSVAPA.....INTCTGEVHERRESFLARAN 93 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

283224 seqs, 96134422 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_73:\* Database

piri:\* pir2:\* pir3:\* pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

4		æ (			SUMMARIES	
Result No.	Score	Query	Query Match Length	DB	ID	Description
1	92.5	18.1	196	7	5.4	The state of the s
7	92.5	18.1	259	~	T52619	
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7 .	200	15.7	133		T09608	environmental stre
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4.	79	15.5	204		T09592	
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16	77	15.1	754		JC4898	
17	76.5		77		T16436	u ק
18	76.5	S	332		C83682	
19	92	14.9	102		130119	
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73.5 73.5 73.5 73.5 72.7 71.5 71.5 71.5	71 70.5
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## ALIGNMENTS

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TINY-like protein [imported] - Arabidopsis thaliana
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
C; Accession: G8443
R; anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sp A; Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A; Reference number: A85001; MUID:20083488; PMID:10617198
A; Actual: preliminary
A; Molecule type: DNA
A; Residues: 1-196 <STC>
                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:NC_001268; NID:97270639; PIDN:CAB80356.1; GSPDB:GN00140 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Map position: 4
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Query Match 18.1%; Score 92.5; DB 2; Length 196; Best Local Similarity 33.8%; Pred. No. 0.012; Matches 24; Conservative 12; Mismatches 24; Indels 11; Gaps

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21 GFGRHGGG-VQQHVVKEKFEE----VDTVSRAGA---NHHHHGH-HGGHGFVVRET--R 69 ò g

70 VEEDINTCTGE 80 ð

::|: |:: 159 INDDLMECSSK 169

g

RESULT 2

TINY-like protein [imported] - Arabidopsis thaliana (fragment)
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 24-Oct-2000 #sequence\_revision 24-Oct-2000 #text\_change 24-Oct-2000
C.Accession: T52619
R.Terryn, N.; Heijnen, L.; De Keyser, A.; Van Asseldonck, M.; De Clercq, R.; Verbakel ueller, C.; Mayer, K.; Dehalis, P.; Rombauts, S.; Van Montagu, M.; Rouze, P.; Vos, P.
A.Reference number: 226022; MUID:99192287; PMID:10094464
A.Recession: T52619
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Status: preliminary;
A.Molecule type: mRNA
A.Residues: 1-259 <TER>
A.Cross-references: EMBL:AJ002598; PIDN:CAA05630.1

A; Map position: 4

**Ouery Match** 

hypothetical prote

18.1%; Score 92.5; DB 2; Length 259;

Length 1245;

DB 2; 0.21;

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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1245 <SCH>
A;Cross-references: EMBL:AL356815; GSPDB:GN00116; NCSP:B24H17.10
A;Experimental source: BAC clone B24H17; strain OR74A
C;Genetics:
A;Gene: NCSP:B24H17.10
A;Map position: 6
A;Introns: 6/2; 1141/3
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Pred. No. C
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72.2%;
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Best Local Similarity 34.8
Matches 24; Conservative
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Best Local Similarity 72.2
Matches 13; Conservative
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A; Molecule type: DNA
A; Residues: 1-473 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A. Accession: A42055
A. Accession: A42055
A. Accession: A42055
A. Accession: A42055
A. Accession: A42055
A. A. Accession: A52055
A. A. Cross-references: GB-M3963; NID:g202270; PIDN: AAA40522.1; PID:g202271
A. Cross-references: GB-M3963; NID:g202270; PIDN: AAA40522.1; PID:g202271
A. Cross-references: GB-M3963; NID:g202271
A. Cross-reference extracted from NCBI backbone (NCBIN:74641, NCBIP:74642)
B. Hariharan, N.; Kelley, D.E.; Perry, R.P.
A. Aritle: Gelta, a transcription factor that binds to downstream elements in several poly A. Reference number: A56418; MUID:92052178; PMID:1946404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: A48273
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-414 <RES>
A;Cross-references: GB:L13968; NID:g293847; PIDN:AAA40477.1; PID:g293849
A;Cross-references: GB:L13968; NID:g293847; PIDN:AAA40477.1; PID:g293849
B;Flanngan, J.R.; Becker, K.G.; Ennist, D.L.; Gleason, S.L.; Driggers, P.H.; Levi, B.Z.;
MOI. Cell. Biol. 12, 38-44, 1992
A;Title: Cloning of a negative transcription factor that binds to the upstream conserved
A;Reference number: A42055; MUID:92107191; PMID:1309593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Safrany, G.; Perry, R.P.
Proc. Natl. Acad. Sci. U.S.A. 90, 5559-5563, 1993
A;Title: Characterization of the mouse gene that encodes the delta/YY1/NF-E1/UCRBP trans
A;Reference number: A48273; MUID:93296177; PMID:8516301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7
                                                                                                                            21 GFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHHGHHGGHGFVVRETRVEEDINTCTGE 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69
                                                                                                                                                                                                                                                                                                                                                                                                                  C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 01-Dec-2000
C:Accession: A48273; A42055; A56418
                                                                                                21 GFGRHGGG-VQQHVVKEKFEE----VDTVSRAGA---NHHHHHGH-HGGHGFVVRET--R
                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-218, 'S',220-374,'G',376-414 <HAR>
A;Residues: 1-218, 'S',220-374,'G', NID:9192940; PIDN:AAA37521.1; PID:9192941
A;Cross-references: GB:M74590; NID:9192940; PIDN:AAA37521.1; PID:9192941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16;
                                              11;
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                                              24; Indels
                                                                                                                                                                                                                                                                                                                                                                                               delta/YY1/NF-E1/UCRBP transcription factor - mouse
                        0.016;
                        Pred. No. 0.01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: ub:m,w,v, c;Genetics:
C;Genetics:
A;Introns: 227/1; 281/2; 301/3; 354/3
C;Keywords: transcription factor; zinc finger
                                                    12;
                           33.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55 GGGDHGGGGGGH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         || :| | :
99 VHHHQEVILVQ 109
                                                    Conservative
                                                                                                                                                                                                                                                             222 INDDLMECSSK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 VHERRESFLAR 91
                                                                                                                                                                                                            70 VEEDINTCTGE 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
nes 22; Conserv
                           Similarity
24; Conserv
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                           Best Local
Matches 2
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Matches
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C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C; Accession: D96591
C; Accession: D96591
C; Accession: D96592
C; Arabidopsis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, Chin, C.W.; Chung, M.K.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; V.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.W.; Sun, H.; Tallo A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.W.; Sun, H.; Tallo A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rypauley, A.; Scheet, P.; Harper, M.

submitted to the EMBL Data Library, February 1999
A; Description: The Sequence of C. elegans cosmid W03G1.
A; Reference number: Z21454
A; Accession: T3397
A; Reference number: L3397
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-471 < PAU>A; Craule type: DNA
A; Residues: L471 < PAU>A; Craule type: Company C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T33997
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Gaps
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Indels
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             2; Mismatches
                                                                                                                                                                                                                                                              918
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Gaps

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A;Cross-references: EMBL:U23523; NID:9746551; PID:9746557; PIDN:AAC46561.1; CESP:F53A
A;Experimental source: strain Bristol N2
                                                                                                                                                                                                                                                                                             Transcription factor Brn-1 - mouse
N.Alternate names: class III POU domain protein brain-1
C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Accession: S31233
E.Accession: S31233
F.Hara, Y.; Rovescall, A.C.; Kim, Y.; Nirenberg, M.
Froc. Natl. Acad. Sci. U.S.A. 89, 3280-3284, 1992
A.Title: Structure and evolution of four POU domain genes expressed in mouse brain.
A.Reference number: S31223; MUID:92228768; PMID:1565620
A.Reference number: S31223; A.Structure and evolution of four POU domain genes expressed in mouse brain.
A.Reference number: S31223; MUID:92228768; PMID:1565620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-495 < HAR>
A; Residues: 1-495 < HAR>
A; Residues: 1-495 < HAR>
A; Cross-references: EMBL: M88299; NID: g200444; PIDN: AAA39960.1; PID: g200445
C; Superfamily: transcription factor Brn-1; homeobox homology; POU domain homology
C; Keywords: DNA binding; homeobox; nucleus; transcription regulation
E; 27-49/Region: glycine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein F53A9.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: Ti6437
                                                                                                                                                             Length 495;
                                                                                                                             19 PAGFGRHGGGVQQHVVKEKFEEVDTVSRAGA----NHHHHHHHHHGHHGGHGF
                                     Length 173;
                                                                                  15; Indels
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Pred. No. 0.089;
5; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Willer, N.
submitted to the EMBL Data Library, March 1995
A;Description: The sequence of C. elegans cosmid F53A9.
A;Reference number: Z18513
A;Recession: T16437
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule Preliminary; translated from GB/EMBL/DDBJ
A;Molecule Yrpe: DNA
A;Residues: 1-86 <MIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36;
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                          16.1%; Score 82; DB 2; 34.7%; Pred. No. 0.15; 1ve 7; Mismatches 1
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26.1%; Pred. No. 0.5;
tive 7; Mismatches
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F)267-291/Region: histidine/proline-rich
F)316-383/Domain: POU domain homology <POI
F)402-458/Domain: homeobox homology <HOX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;101-112/Region: alanine-rich
F;162-180/Region: histidine/proline-rich
F;186-201/Region: alanine-rich
F;236-247/Region: glycine-rich
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Best Local Similarity 29.5%;
Matches 23; Conservative
                     Query Match
Best Local Similarity 34.79
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 16.0%
Best Local Similarity 26.1%
Matches 24; Conservative
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A;Gene: CESP:F53A9.6
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                                                                                                                                                                                                                                                                                                                                             RESULT 7
T45059
hypothetical protein X39B6B.gg [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C;Accession: T45059
R;Wilson, R.; Ainscough, R.; Anderson, K.; Baynes, C.; Berks, M.; Bonfield, J.; Burton, raser, A.; Fulton, L.; Gardner, A.; Green, P.; Hawkins, T.; Hillier, L.; Jier, M.; Johns Nature 36B, 32-38, 1994
A;Authors: Shownkeen, R.; Sims, M.; Smaldon, N.; Smith, A.; Smith, M.; Sonnhammer, E.; S A;Title: 2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.
A;Reference number: 843531; MUID:94180718; PMID:7906398
A;Eccession: T45059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycine/prolline-rich protein - Arabidopsis thaliana
N.Alternate names: protein K10A8_130
C. Species: Arabidopsis thaliana (mouse-ear cress)
C. Species: Arabidopsis thaliana (mouse-ear cress)
C. Accession: T51469
R. Sato. S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.; Mew A; Reference number: Z23394
A; Accession: T51469
A; Reference number: Z23394
A; Accession: T51469
A; Status: preliminary
A; Another and A; Residues: 1-173 <SAT>
A; Residues: 1-173 <SAT>
A; Residues: 1-173 <SAT>
A; Residues: 1-173 <SAT>
A; Cross-references: EMBL:Al391151
A; Experimental source: cultivar Columbia; BAC clone K10A8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AE005173; NID:99857523; PIDN:AAG00878.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53
                                                                                                                                                                                                                                                                DYCSEEVRSVAPAGFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHGH----HGGH 61
                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 735;
                                                                                                                                          Length 473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                     ; Score 84; DB 2;
; Pred. No. 0.26;
10; Mismatches
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26.4%; Pred. No. 0.6;
iive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A Molecule type: DNA
A; Residues: 1-735 <WIL>
A; Cross-references: EMBL:AL132896; N
A; Experimental source: clone Y3986B
                                                                                                                             16.5%;
36.8%;
                                                                                                Query Match
Best Local Similarity 36.00,
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563 SLAHHGHHGGHG 674
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Best Local Similarity
Matches 19; Conserv
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                        C;Genetics:
A;Gene: T24C10.10
A;Map position: 1
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A;Introns: 18/1; 6
A;Note: Y39B6B.gg
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A; Introns: 97/1
A; Note: K10A8_130
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25; Gaps

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56;

-----GVQQHVVKEKFEEVDTVS 45

1 MAYYQEVDYCSEEVRSVAPAGFGRHGG------

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Transcription repressor protein YYI - human N; Alternate names: transcription repressor/activator protein NF-E1 N; Alternate names: transcription repressor/activator protein NF-E1 C; Species: Homo sapiens (man) C; Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 08-Oct-1999 C; Accession: A40390; S78494; S33712; A56419 F; Shi, Y; Seto, E; Chang, L.S.; Shenk, T. Cell 67, 377-388, 1991 A; Title: Transcriptional repression by YYI, a human GLI-Krueppel-related protein, and A; Title: Transcriptional repression by YYI, a human GLI-Krueppel-related protein, and A; Title: Transcriptional repression by YYI, PMID:1655281
                                                                                                                        genes. IX. The comp
                                                                          Nomura, N.; Ohara,
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C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000
C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000
C;Accession: 100338
R;Magase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; C
DNA Res. 5, 31-39, 1998
A;Title: Prediction of the coding sequences of unidentified human genes. IX. Th
A;Reference number: Z14086; MUID:98290545; PMID:9628581
A;Recession: T00338
A;Recente number: Z14086; MUID:98200545; PMID:9628581
A;Recenter number: Z14086; MUID:9304365; PMID:9628581
A;Residues: 1-1273 <NAG>
A;Residues: 1-1273 <NAG>
A;Residues: 1-1273 <NAG>
A;Residues: 1-1273 <NAG>
C;Genetics: EMBL:AB011142; NID:93043663; PIDN:BAA25496.1; PID:93043664
A;Experimental source: brain; clone HH2365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---H 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein corA, cold- and drought-regulated - alfalfa
C;Species: Medicago sativa (alfalfa)
C;Species: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: EMBL:L03708; NID:g289122; PIDN:AAA99833.1; PID:g289123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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A;Molecule type: mRNA
A;Residues: 1.414 <SHI>
A;Cross.references: GB:M77698; NID:g186767; PIDN:AAA59467.1; PID:g186768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48 GANHHHHHHHHGHH--GFVVRETRVEEDINTCTGEVHERRESFLA 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rilaberge, S.; Castonguay, Y.; Vezina, L.P.
Plant Physiol. 101, 1411-1412, 1993
A; Title: New cold- and drought-regulated gene from Medicago : A; Reference number: 216754; MUID:94143496; PMID:8310076
A; Accession: T09592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 GFGRHGGGVQQHV-VKEKFEEVDTV-----SRAGANH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24;
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                                                                                                                                                                                                                                                                                                                                                      A; Note: KIAA0570
C; Superfamily: human hypothetical protein KIAA0570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.37;
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C;Superfamily: Arabidopsis glycine-rich protein 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15.5%; Score 79;
ilarity 30.4%; Pred. No. C
Conservative 3; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 80;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                        15.7%;
ilarity 33.3%;
Conservative
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Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A: Residues: 1-204 <LAB>
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Best Local Simi
Matches 24;
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                                                                                                                                                                                                                                                     C; Species: wedicago sativa (alfalfa)
C; Species: Medicago sativa (alfalfa)
C; Species: Medicago sativa (alfalfa)
C; Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C; Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C; Accession: A42844
R; Luo, M.; Liu, J. H.; Mohapatra, S.; Hill, R.D.; Mohapatra, S.S.
J. Biol. Chem. 267, 15367-15374, 1992
J. Biol. Chem. 267, 15367-15374, 1992
A; Tatle: Characterization of a gene family encoding abscisic acid- and environmental stransference number: A42844; MUID:92346382; PMID:1379227
A; Accession: A42844
A; Molecule type: mRNA
A; Residues: 1-191 < LUO>
A; Residues: 1-191 < LUO>
A; Cross-references: GB:S40947; NID:9252396; PIDN:AAB22713.1; PID:9252397
A; Note: sequence extracted from NCBI backbone (NCBIN:109886, NCBIP:109889)
C; Superfamily: Arabidopsis glycine-rich protein 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: T09608
R; Luo, M.; Mohapatra, S.; Hill, R.
submitted to the EMBL Data Library, February 1992
A; Description: Nucleotide sequence analysis of a environmental stress and ABA inducible A; Reference number: 216770
A; Accession: T09608
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                         environmental stress-induced protein - alfalfa (fragment)
C;Species: Medicago sativa (alfalfa)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 02-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24; Gaps
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A; Residues: 1-13.
A; Cross-references: EMBL:M74190; NID:g166373; PID:g166374
A; Experimental source: cultivar Anik
C; Superfamily: Arabidopsis glycine-rich protein 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
0.21;
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pred. No. 0.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 81; DB
Pred. No. 0.21
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          153 GGHGGHGADQTEDNTQNDHN 175
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hypothetical protein KIAA0570 - human
                                                                                                                                  46 RAGANHH--HHHGHHGGH 61
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nilarity 28.7%;
Conservative 8
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30.1%;
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Best Local Similarity 30.1
Matches 25, Conservative
                                 Query Match
Best Local Similarity
Matches 27; Conserv
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A:Experimental source: HeLa cells
A:Note: the authors translated the codon CGC for residue 371 as Lys, CGA for residue 375
R;Whitson, R.H.; Huang, T.; Dang, J.; Itakura, K.
submitted to the EMBL Data Library, July 1992
A:Description: Observed and predicted DNA binding of a zinc finger protein which recognia, A:Reference number: S78494
                                                                                                                                                                                                        A; Wolecule type: mRNA
A; Readdues: 1-195,'G',197-414 <WHI>
A; Cross-references: EBL214077; NID:g38010; PIDN:CAA78455.1; PID:g38011
R; Park, K; Atchison, M.L.
Proc. Natl. Acad. Sci. U.S.A. 88, 9804-9808, 1991
A; Title: Isolation of a candidate repressor/activator, NF-E1 (YY-1), delta, that binds
A; Accession: S33712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 GFGRHGGGVQQHVVKEKFEEVDTVSRACANHHHHHGHHGGH-GFVVRETRVEEDINTCTG 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                               A Molecule type: mRNA

A Mesiduaes: 1-64, R', 66-195, 'G', 197-414 <PAR>
A: Residuaes: 1-64, R', 66-195, 'G', 197-414 <PAR>
A: Cross-references: GB:M76541; NID:g189173; PIDN:AAA59926.1; PID:g189174
C; Keywords: DNA binding; transcription regulation; zinc finger
C; Keywords: DNA binding; transcription regulation; zinc finger
E; 328-347/Region: zinc finger CCHH motif
F; 335-377/Region: zinc finger CCHH motif
F; 385-407/Region: zinc finger CCHH motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20;
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Pred. No. 0.78;
6; Mismatches 25; Indels
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Best Local Similarity 29.2%;
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55 GGGDHGGG-----
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96 QVHHHQEVILVQ 107
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OM protein - protein search, using sw model

June Run on:

6, 2003, 12:42:32; Search time 13 Seconds (without alignments) 296.715 Million cell updates/sec

US-10-090-035-2 510 1 MAYYQEVDYCSEEVRSVAPA.....INTCTGEVHERRESFLARAN 93 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

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1 TYX1 MOUSE						1 DYRA_HUMAN	1 DYRA_MOUSE	DYRA_RAT	MAK_HUMAN	L CDA4_ACUSE	Cox amax	THAT AVICA	Cant One	2.281 HIMAN	CCAD CHICK	VV59 CARRI	EP84 HCMVA	GAB DROME	SNF1 YEAST	OTX1_HUMAN	A2AC DIDMA	ZICZ HUMAN	SRCH HUMAN	FSH DROME	SALA DROST	OTX1 MOUSE	OTX1 PAT	CCT1 HORSE	HMCU DROME	HUNB DROCK	MAF_MOUSE
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	92 18.0 414 1 TYY1 MOUSE	92 18.0 414 1 TYY1_MOUSE Q00899 81.5 16.0 495 1 BRN1_MOUSE	92 18.0 414 1 TYY1_MOUSE 000899 mus 81.5 16.0 495 1 BRN1_MOUSE P31361 mus 81.5 16.0 497 1 BRN1_RAT 063267 254	92 18.0 414 1 TYYL MOUSE 000899 81.5 16.0 495 1 BRNL MOUSE P31361 81.5 16.0 497 1 BRNL RAT Q63262 80.5 15.8 500 1 BRNL HUMAN	92 18.0 414 1 TYYL MOUSE Q00899 81.5 16.0 495 1 BRNL MOUSE P31361 81.5 16.0 497 1 BRNL RAT Q63262 80.5 15.8 500 1 BRNL HUAN P20284 79 15.5 204 1 CORA, MEDSA	92 18.0 414 1 TYY1_MOUSE 000899 81.5 16.0 495 1 BRN1_MOUSE P31361 81.5 16.0 497 1 BRN1_RAT 063262 80.5 15.8 500 1 BRN1_HUMAN P20264 79 15.5 204 1 CORA_MEDSA 007202 79 15.5 414 1 TYY1_HUMAN P26490	2 18.0 414 1 TYY1_MOUSE 000899 5 16.0 495 1 BRN1_MOUSE P31361 5 16.0 497 1 BRN1_RAT 063362 5 15.8 500 1 BRN1_HUMAN P20264 9 15.5 204 1 CORA_MEDSA 007202 7 15.1 763 1 DYRA_HUMAN P25490	92 18.0 414 1 TYYL MOUSE 000899 81.5 16.0 495 1 BRNL MOUSE 81.5 16.0 497 1 BRNL MOUSE 05362 80.5 15.8 500 1 BRNL HUMAN P20264 79 15.5 204 1 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1 CCAD_CHICK P7187 73 14.3 604 1 CCAD_CHICK P7187 73 14.3 604 1 CCAD_CHICK P7187 74 14.5 606 1 GAB_DRONE P55123 P7187 75 14.0 653 1 ZICZ_HUMAN P52327 P7372 71.5 14.0 653 1 ZICZ_HUMAN P52337 P73727 71 13.9 2038 1 ESH DRONE	92 18.0 414 1 TYYL_MOUSE  81.5 16.0 495 1 BRN1_MOUSE  80.5 15.8 500 1 BRN1_HOMAN  70 15.5 204 1 CORA_MEDSA  70 15.5 204 1 TYYL_HUMAN  71 15.1 763 1 DYRA_HUMAN  72 15.1 763 1 DYRA_HRAT  73 14.9 403 1 MAR_HUMAN  74 14.5 51 1 DYRA_HUMAN  75.5 14.8 425 1 DYRA_HUMAN  75.5 14.8 425 1 DOUL_BRARE  76 14.9 403 1 MAR_HUMAN  77 15.1 763 1 DYRA_RAT  78 14.8 558 1 CBR4_HUMAN  79 15.5 14.8 558 1 CBR4_HUMAN  71 14.5 2190 1 CGAD_CHICK  72 14.4 684 1 CSUP_DROME  73 14.4 684 1 CSUP_CHICK  73 14.4 684 1 CYSQ_CAEEL  74 14.5 2190 1 CGAD_CHICK  75 14.4 684 1 AAAC_LOIDMA  76 14.0 699 1 SRCH_HUMAN  71.5 13.9 20.8 1 SRCH_HUMAN	92 18.0 414 1 TYYL_MOUSE  81.5 16.0 495 1 BRNL_MOUSE  80.5 15.8 504 1 GORA_MEDSA  79 15.5 204 1 GORA_MEDSA  79 15.5 204 1 GORA_MEDSA  70 15.1 763 1 DYRA_MUNN  71 15.1 763 1 DYRA_MUNN  72 14.9 551 1 GRA_MOUSE  75.5 14.8 452 1 GRA_MOUSE  75.5 14.8 551 1 GRA_MOUSE  75.5 14.8 521 1 GRA_MOUSE  76 14.9 551 1 GRA_MOUSE  77 15.1 763 1 DYRA_RAT  78 14.8 521 1 GRA_MOUSE  78 14.7 369 1 TWAF_AVIS4  79 14.5 2190 1 CCAD_CHICK  79 14.5 2190 1 CCAD_CHICK  71 14.5 2190 1 GAB_DROME  71 14.5 606 1 GAB_DROME  72 14.4 1 GRA_MOUSE  73 14.3 606 1 GAB_DROME  74 14.5 2190 1 GAB_DROME  75 14.0 469 1 SRCH_LHUMAN  71.5 14.0 699 1 SRCH_LHUMAN  71.5 14.0 699 1 SRCH_LHUMAN  71.5 14.0 699 1 SRCH_LHUMAN  71.5 13.9 2038 1 FSH_DROME  70.5 13.8 13.9 1 GYXL_MOUSE  70.5 13.8 1	92 18.0 414 1 TYYL_MOUSE  81.5 16.0 495 1 BRNL_MOUSE  80.5 15.0 497 1 BRNL_RAT  80.5 15.0 497 1 BRNL_RAT  80.5 204 1 CORA_MEDSA  70 15.5 204 1 CORA_MEDSA  71 15.1 763 1 DYRA_HUMAN  72 15.1 763 1 DYRA_HUMAN  73 15.1 763 1 DYRA_HOUSE  74 14.9 40.0 55.1 1 CRA_HOUSE  75.5 14.8 425 1 CRA_HOUSE  75.5 14.8 425 1 CRA_HOUSE  75.5 14.8 425 1 CRA_HOUSE  75.5 14.8 625 1 CRA_HOUSE  76 14.9 551 1 CRA_HOUSE  77 15.1 763 1 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SRCH_HUMAN 92.077 92.1 4.9 606 1 SRCH_HUMAN 92.077 92.1 4.9 608 1 SRCH_HUMAN 92.077 92.1 3.9 20.38 1 SALA_DROME 92.077 92.1 3.8 355 1 OTXI_MOUSE 92.077 92.1 3.8 355 1 OTXI_MOUSE 92.077 92.1 3.8 355 1 OTXI_MOUSE	92 18.0 414 1 TYYL_MOUSE  81.5 16.0 495 1 BRNL_MOUSE  80.5 15.8 504 1 GORA_MEDSA  79 15.5 204 1 GORA_MEDSA  79 15.5 204 1 GORA_MEDSA  70 15.1 763 1 DYRA_MOUSE  70 15.1 763 1 DYRA_MOUSE  71 15.1 763 1 DYRA_MOUSE  72 14.9 551 1 GRA_MOUSE  73 14.9 551 1 GRA_MOUSE  74 14.5 14.0 40.0 1 GORA_MOUSE  75 14.7 36.9 1 TWAF_AVISA  76 14.9 551 1 GRA_MOUSE  77 14.7 36.9 1 TWAF_AVISA  78 14.7 36.9 1 TWAF_AVISA  79 14.5 2190 1 CCAD_CHICK  70 14.5 2190 1 CCAD_CHICK  71 14.5 2190 1 CCAD_CHICK  72 14.4 14.5 2190 1 CCAD_CHICK  73 14.3 606 1 GAB_DROME  74 14.5 2190 1 GORA_MOUSE  75 14.0 46.9 1 AZAC_DIDMA  76 14.9 521 2 GORA_MOUSE  77 14.1 354 1 OTXL_LHUMAN  78 14.3 606 1 GAB_DROME  79 14.0 699 1 SRCH_LHUMAN  70 5 13.8 13.9 1 SRCH_LHUMAN  71 13.9 2038 1 FSH_DROME  70 5 13.8 13.5 1 OTXL_RAF  70 7 7 7 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Q9xtq7 caenorhabdi P51022 drosophila 060563 homo sapien 0608617 sarcophaga P40764 mus musculu 018879 caenorhabdi P24345 zea mays (m 013934 mus musculu 063934 nomo sapien 063934 nos sapien 063934 pomo sapien 099591 drosophila
KE4L_CAEEL PNT1_DROME CCT1_HUMAN ANTE_SARPE DIX2_MOUSE CAV2_CAEEL HRN1_MAIZE BR3B_HUMAN BR3B_HUMAN RX_DROME HRPX_PLALO
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4888 4444 44 44 44 44 44 44 44 44 44 44

## ALIGNMENTS

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Proc. Natl. Acad. Sci. U.S.A. 89:3280-3284(1992).
-!- SUBCELLULAR LOCATION: Nuclear.
-!- TISSUE SPECIFICITY: BRAIN.
-!- SIMILARITY: BELONGS TO THE POU TRANSCRIPTION FACTOR FAMILY.
                                                                                CLASS-3 SUBFAMILY.
-!- SIMILARITY: CONTAINS 1 HOMEOBOX DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POLY-ALA.
POLY-ALA.
HIS-RICH.
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                                                                                                                                                                                                                                                                                                                                                                                 Principle of the property of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                             PIR; S31223; S31223.
HSSP; P14859; 10CT.
MGD; MG1:102564; Pou3f3.
InterPro; IPR001356; Homeobox.
InterPro; IPR00327; POU_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1998 (Rel. 36, Created)
15-JUL-1999 (Rel. 38, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00035; POU_1; 1.
PROSITE; PS00465; POU_2; 1.
Nuclear protein; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50012 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16.0%;
26.1%;
                                                                                                                                                                                                                                                                            EMBL; M88299; AAA39960.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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Best Local Similarity
Matches 24; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   495 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BRN1_RAT
Q63262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA_BIND
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TANNIERAC; TOUBDD;

R MGD; MGI:99150, Yyl.

R InterPro; IPRO00822; Znf_C2H2.

R Pfam: PF000096; zf-C2H2; 4.

DR PRINTS; PR000048; ZINCFINGER.

DR PRODOM; PD000003; Znf_C2H2; 1.

DR PROSITE; PS00026; ZINC_FINGER_C2H2_1; 4.

DR PROSITE; PS00157; ZINC_FINGER_C2H2_2; 4.

DR PROSITE; PS00157; ZINC_FINGER_C2H2_2; 4.

TRANSCRIPC; MCHAILON; REPRESSOY; ACLIVATOR; Nuclear protein; KW Transcription regulation; Repressor; Activator; Nuclear protein; KW Zinc_finger; McHallohiding; Repeat.

Zinc_finger; McHallohiding; DNA-binding; Repeat.

TOURSER STANSCRIPC.

GLY-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE-92228768; Pubmed=1565620; Ambline-92228768; Pubmed=1565620; Hara Y., Rovescalli C., Kim Y., Nirenberg M.; Structure and evolution of four POU domain genes expressed in mouse brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C2H2-TYPE.
C2H2-TYPE.
INVOLVED IN NUCLEAR MATRIX ASSOCIATION
(BY SIMILARITY).
INVOLVED IN REPRESSION OF ACTIVATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSCRIPTION (BY SIMILARITY).
INVOLVED IN MASKING TRANSACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUL-1993 (Rel. 26, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Brain-specific homeobox/POU domain protein 1 (BRN-1 protein).
POUJST3 OR OTF8.OR BRNI OR BRN-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 92; DB 1; Length 414;
Pred. No. 0.017;
7; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN (BY SIMILARITY).
F -> S (IN REF. 3).
R -> G (IN REF. 3).
C012378288E984F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        495 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLY-HIS.
GLY/SER-RICH.
ZINC FINGERS.
C2H2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7; Mismatches
                      email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                        01-JUL-1993 (Rel. 26, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44717 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 18.0%;
Best Local Similarity 31.0%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                         EMBL; M73963; AAA40522.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1| :| | :
99 VHHHQEVILVQ 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81 VHERRESFLAR 91
                                                                                  AAA40477.1
                                                                            AAA40477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 375 ... 414 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                           RANSFAC; T00278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         333
                                                                                                                                                                                      P25490;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BRN1_MOUSE
P31361;
                            an
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ZN_FING
ZN_FING
ZN_FING
ZN_FING
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19 PAGFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHH-------GHHGGHG- 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ς:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-98070400; PubMed-9405434;
Schreiber J., Enderich J., Sock E., Schmidt C., Richter-Landsberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Brain-specific homeobox/POU domain protein 1 (BRN-1 protein).
POUJS OR BRN1 OR BRN-1 OR RHS2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Redundancy of class III POU proteins in the oligodendrocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 495;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HOMEOBOX.
77B802E890C9A014 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 81.5; DB 1;
Pred. No. 0.26;
7; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         297 GPGLNSHDPHSDEDTPTSDDLEQFAKOFKQRR 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 -----FVVRETRVEEDINTCTGEVHERR 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 497 AA
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FRANSFAC; T04469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nuclear protein;
                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                  ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      le Moine C., Young W.S., "RHS2, a POU domain-containing gene, and its expression in developing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 PAGFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHH--------GHHGGHG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                       25;
                                                                                                               -1- SIMILARITY: BELONGS TO THE POU TRANSCRIPTION FACTOR FAMILY. CLASS-3 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 497;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              00640505E343ABC2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            299 GPGLNSHDPHSDEDTPTSDDLEQFAKQFKQRR 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26.1%; Pred. No. 0.26; ive 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 -----FVVRETRVEEDINTCTGEVHERR 85
                                                                                                                                -1- SIMILARITY: CONTAINS 1 HOMEOBOX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 81.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         200
       Biol. Chem. 272:32286-32293(1997).
                                                                                                                                                                                                                                                                                                                                                                                           POLY-ALA.
POLY-GLY.
POLY-HIS.
POLY-GLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                      HOMEOBOX
                                 TISSUE-Hypothalamus;
MEDLINE-92228769; PubMed-1348858;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                         PRO0028; POUDOMAIN.
PD000010; Homeobox; 1.
PD000583; POU_domain; 1.
                                                                                                                                                                                                                                         InterPro: IPR001356; Homeobox.
InterPro: IPR001327; POU_domain.
Pfam; PP001046; homeobox; 1.
Pfam; PP00157; Pou; 1.
PRINTS; PR001028; POUDOMAIN.
                                                                                                                                                                                                                                                                                                                ROSITE; PS00027; HOMEOBOX_1; 1.
ROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                  249 PO
280
301 PO
385 PO
462 HO
50226 MW;
                                                                                                                                                                                                                EMBL; AJ001641; CAA04893.1; -.
EMBL; M84644; AAA42041.1; -.
HSSP; P14859; 10CT.
                                                                                                                                                                                                                                                                                                                           PROSTIE; PSOUGAS, POUL; 1.
PROSTIE; PSO0465; POUL2; 1.
Nuclear protein; DNA-binding;
                         SEQUENCE OF 325-449 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BRNI_HUMAN STANDARD;
P20264; P78379;
01-FEB-1991 (Rel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            16.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 26.1
24; Conservative
                                                                                                                                                                                                                                                                                                   SMART; SM00389; HOX; 1
SMART; SM00352; POU; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                   403
497 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 24
                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                         PROSITE;
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                                                                                                                                                                        [1]
SEQUENCE FROM N.A.
MEDLINE-96359175; PubMed-8703082;
MEDLINE-96359175; PubMed-8703082;
MEDLINE-96359175; PubMed-8703082;
SUMLYAMA K., Washlo-Watanabe K., Saltou N., Hayakawa T., Ueda S.;
"Class III POU genes: generation of homopolymeric amino acid repeats under GC pressure in mammals.";
under GC pressure in mammals.";
                                                                                                         Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
Brain-specific homeobox/FOU domain protein 1 (BRN-1 protein).
POU3F3 OR BRN1 OR OTP8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -> S (IN REF. 2).
E536EFFFA5212319 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- SIMILARITY: CONTAINS 1 HOMEOBOX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PSU002;
PS00035; POU_1; 1.
PS00465; POU_2; 1.
PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLY-GLY.
POLY-ALA.
POLY-PRO.
POLY-PRO.
POLY-ALA.
POLY-GLY.
HIS-RICH.
POLY-HIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POU.
HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Brain;
MEDLINE-89295573; PubMed-2739723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001356; Homeobox.
InterPro; IPR000327; POU_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRO0028; POUDOMAIN.
PD000010; Homeobox; 1.
PD000583; POU_domain; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS00035; POU_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AB001835; BAA19459.1; -. PIR; SOS042; SO5042.
HSSP; P14859; 10CT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50327 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00046; homeobox; 1.
Pfam; PF00157; pou; 1.
PRINTS; PR00028; POUDOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genew; HGNC:9216; POU3F3.
MIM; 602480; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProDom; PD000583; POU_CSMART; SM00389; HOX; I SMART; SM00352; POU; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                281
304
388
465
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500 AA;
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CONFLICT
SEQUENCE
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DB 1; Length 500;

Score 80.5;

15.8%;

Query Match

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53 HHHGHHGGHGFVVRETRVE 71
                                                                                                                                                                                                                                                                                                                                                                                                 nitiator
                                               TYY1_HUMAN
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                g
                                                                                                                                                                                                                                               between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics in There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                  --- СННССНС 62
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                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolleae; Medicago.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
            Gaps
                                                                                                                                                                                              28;
            15;
                                                                                                                                                                                                                                                                                                                          6 AA REPEATS OF Y-N-H-G-G-G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 79; DB 1; Length 204;
Pred. No. 0.19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 GFGRHGGGVQQHV-VKEKFEEVDTV------SRAGANH-----
                          19 PAGFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHH-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24; Indels
                                                                                                                                                                                                                                                                                                                                                                          11 X 3 AA REPEATS OF H-G-G.
2-1.
             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8A2C082359FCC17F CRC64;
            22;
                                                                                                  01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
Cold and drought-regulated protein CORA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 0.15
3; Mismatches
                                                                             204 AA
      Pred. No. 0.34
; Mismatches
                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                        2-5-5-
2-4-
2-9-
                                                                                                                                                                                    STRAIN-cv. Apica;
MEDLINE-94143496; Pubmed-8310076;
             5
                                                                                          01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last seq
01-FEB-1995 (Rel. 31, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19599 MW;
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       33.9%;
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                                                                                                                                 (Alfalfa)
                                                                                                                                                                                                                                                                                                                      Repeat
             Conservative
                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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      Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                     Multigene family;
                                                                                                                                  Medicago sativa
                                                                                                                                                            NCBI_TaxID=3879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24;
                                                                               CORA_MEDSA
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Matches
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J. MOLL. BIOL. 279:973-986(1998).

J. MOLL. BIOL. 279:973-986(1998).

FUNCTION: MULTIFUNCTIONAL TRANSCRIPTION FACTOR THAT EXHIBITS
POSITIVE AND NEGATIVE CONTROL ON A LARGE NUMBER OF CELLULAR AND VIRAL GENES BY BINDING TO SITES OVERLAPPING THE TRANSCRIPTION START SITE. MAY PLAY AN IMPORTANT ROLE IN DEVELOPMENT AND DIFFERENTIATION. THE FUNCTION OF YYL AS AN ACTIVATOR OR A REPRESSOR IS SPECIFIED BY THE PRESENCE OF OTHER PROTEINS. FOR EXAMPLE IT ACTS AS A REPRESSOR IN ABSENCE OF ADENOVIRUS ELA PROTEIN BUT AS AN ACTIVATOR IN ITS PRESENCE.

FROTEIN BUT AS AN ACTIVATOR IN ITS PRESENCE.

SUBCELLULAR LOCATION: NUCLEAR. ASSOCIATED WITH THE NUCLEAR MATRIX.

SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C242-TYPE ZINC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDILINE-9815291; PubMed-9493912;
MEDILINE-9815291; PubMed-9493912;
MEDILINE-9815291; PubMed-9493912;
Atchison M.L., Penman S., van Wijnen A.J., Stein G.S.;
Atchison M.L., Penman S., van Wijnen A.J., Stein G.S.;
"Targeting of the YY1 transcription factor to the nucleolus and the nuclear matrix in situ: the Cterminus is a principal determinant for nuclear trafficking.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-98308000; PubMed-9642075;
Viles J.H., Patel S.U., Mitchell J.B.O., Moody C.M., Justice D.E.,
Uppenbrink J., Doyle P.M., Harris C.J., Sadler P.J., Thornton J.M.;
"Design, synthesis and structure of a zinc finger with an artificial
                                                                                                                                                                                                                               TYYI_HUMAN STANDARD; PRT; 414 AA.
P2540; 014935;
01-MAY-1992 (Rel. 22, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCCT-2001 (Rel. 40, Last annotation update)
17-CAT-2001 (Rel. 40, Last nunctation update)
17-CAT-2001 (Rel. 40, Last nunctation update)
18-CAT-2001 (Rel. 40, Last nunctation update)
19-CAT-2001 (Rel. 40, Last nunctation update)
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Houbaviy H.B., Usheva A., Shenk T., Burley S.K.;
"Cocrystal structure of YYl bound to the adeno-associated virus P5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                delta),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-92005716; PubMed-1655281;
Shi Y., Seto E., Chang L.-S., Shenk T.,
"Transcriptional repression by YX1, a human GLI-Kruppel-related protein, and relief of repression by adenovirus ElA protein.";
Cell 67:377-388(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Isolation of a candidate repressor/activator, NF-E1 (YY-1, that binds to the immunoglobulin kappa 3' enhancer and the immunoglobulin heavy-chain mu E1 site.";
Proc. Natl. Acad. Sci. U.S.A. 88:9804-9808(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Whitson R.H., Huang T., Dang J., Itakura K.;
Submitted (JUL-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 93:13577-13582(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 304-414.
                                                                                                                                                                                                                           414 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cell. Biochem. 68:500-510(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Foreskin;
MEDLINE=92052179; PubMed=1946405;
nomo sapiens (numan).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRUCTURE BY NMR OF 353-379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Park K., Atchison M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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NCBI_TaxID=9606;
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                                                                                                                                                              region,
                  ON NEW TRANSPORTED BY SECOND COLOR C
                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                        20; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INVOLVED IN NUCLEAR MATRIX ASSOCIATION.
INVOLVED IN REPRESSION OF ACTIVATED
TRANSCRIPTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INVOLVED IN MASKING TRANSACTIVATION DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DYRALHUMAN STANDARD; PRT; 763 AA.
013627; 092810; 092582; 090NM5;
01.MOV-1997 (Rel. 35, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-CCT-2001 (Rel. 40, Last sequence update)
Dual-specificity tyrosine-phosphorylation regulated kinase 1A
(EC 2.7.1.-) (Protein kinase minibrain homolog) (MNBH) (HP86)
DYRKIA OR DYRK OR WNBH OR MNB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.5%; Score 79; DB 1; Length 414; 29.2%; Pred. No. 0.4; Live 6; Mismatches 7.25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        058C05A0AD2D04E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -> R (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLY-RICH.
POLY-HIS.
ZIUC/SER-RICH.
ZIUC FINGERS.
C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
                                                                                                                                                      EMBL; M77698; AAA59467.1; EMBL; M76541; AAA59926.1; EMBL; Z14077; CAA78455.1; PIR, 440350; A40350; PDB; 1UBD; 23-DEC-96 PDB; 1ZNM; 01-APR-98.
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QVHHHQEVILVQ 107
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                                                                                                                                                                                                                                                                      Genew; HGNC:12856; YY1.
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170
407
320
347
377
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196
114 AA;
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Best Local Similarity
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2N_FING
2N_FING
2N_FING
2N_FING
DOMAIN
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                                                                     Song W.J., Sternberg L.R., Kasten-Sportes C., van Reuren M.L., Chung S.H., Slack A.C., Miller D.E., Glover T.W., Chiang P.W., Lou L., Kurnit D.W.;

"Isolation of human and murine homologues of the Drosophila minibrain gene: human homologue maps to 21q22.2 in the Down syndrome 'critical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., VARIANTS F-415; H-681, AND ALTERNATIVE SPLICING. MEDLINE-99263503; PubMed-10329007; Guimera J., Casas C., Estivill X., Pritchard M.; "Human minibrain homologue (MNBH/DYRKI): characterization, alternative splicing, differential tissue expression, and overexpression in Down
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cloning of a human homolog of the Drosophila minibrain/rat Dyrk gene from 'the Down syndrome critical region' of chromosome 21."; Blochem. Blophys. Res. Commun. 225:92-99(1996).
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (LONG ISOFORM).
MEDLINE-97026291; Pubmed-8872470;
Guimera J., Casas. C., Pucharcos C., Solans A., Domenech A.,
Planas A.M., Ashley J., Lovett M., Estivill X., Pritchard M.A.;
"A human homologue of Drosophila minibrain (MNB) is expressed in the neuronal regions affected in Down syndrome and maps to the critical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1- FUNCTION: MAY PLAY A ROLE IN A SIGNALING PATHWAY REGULATING NUCLEAR FUNCTIONS OF CELL PROLIFERRATION. PHOSPHORYLATES SERINES, THREONINES AND TYROSINES RESIDUS IN ITS SEQUENCE AND IN EXOGENOUS
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-!- ALTERNATIVE PRODUCTS: AT LEAST 5 ISOFORMS; A LONG FORM (SHOWN HERE), I, 2, 3 AND 4; ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- TISSUE SPECIFICITY: UBIGUITOUS. HIGHEST LEVELS IN SKELETAL MUSCLE, TESTIS, FETAL LUNG AND FETAL KIDNEY.
-!- DEVELOPMENTAL STAGE: EXPRESSED IN THE DEVELOPING CENTRAL NERVOUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-96332410; Pubmed-8769099;
Shindoh N., Kudoh J., Maeda H., Yamaki A., Minoshima S., Shimizu Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 1).
Miki O., Masahira H., Yasufumi M., Naohiko S., Takahiro N.,
Hitoshi I., Nobuo N., Toshihiko E., Yoshiyuki S., Misao O.,
Hitoshi M., Seki N., Nagase T., Suzuki E., Nomura N., Ohara O.,
Hattori M., Sakaki Y., Eki T., Murakami Y., Saito T., Ichikawa H.,
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-i- DISEASE: OVEREXPRESSED 1.5-FOLD IN FETAL DOWN SYNDROME BRAIN.
-i- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
MNB/DYRK SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   region.";
Hum. Mol. Genet. 5:1305-1310(1996).
SEQUENCE FROM N.A. (LONG ISOFORM).
MEDLINE-97131512; Pubmed-8975710;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 1). TISSUE-Fetal brain;
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                                                                                                                                                                                                                                                                                                         Genomics 38:331-339(1996).
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D85759;
D86550;
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DYRKIA OR DYRK
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MOD_RES
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                                                                                                                           region'
614
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                                                                                                                                                                                                                                                             GGSSGTSNGGRARSDPTHOHHHSGG -> VEQHWMPGAFRM
TVSFTLEVHDVPV (IN ISOFORM 3).
MISSING (IN ISOFORM 3).
                                                Intertry into transe; I.
Prodom; PP000001; Buk_pkinase; 1.
Prodom; PD000001; Buk_pkinase; 1.
SMART; SM00120; S_TKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
Transferase; Serine/threonine-protein kinase; Tyrosine-protein kinase; ATP-binding; Nuclear protein; Phosphorylation; Alternative splicing;
                                                                                                                                                                                                                                                                                    SSHVVHLLVSP
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SIMILARITY).
SIMILARITY).
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                                                                                                                     BIPARTITE NUCLEAR LOCALIZATION SIGNAL
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PHOSPHORYLATION (AUTO-) (BY SIMILARIT
MISSING (IN ISOFORM 1).
GGSSGTSNSGRARS -> GASAISCSSWIVRH (IN
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15-UUL-1999 (Rel. 38, Last sequence update)
16-UCT-2001 (Rel. 40, Last annotation update)
10-OCT-2001 (Rel. 40, Last annotation update)
bual-specificity tyrosine-phosphorylation regulated kinase 1A
                                                                                                                                                                                                                                                                                     ROOFPAPLGWSGTEAPTOVTVETHPV -> {
ALLRWSSTGCQVPLE (IN ISOFORM 4)
                                                                                                                                                                                                                                                                                                                                                                                                              Score 77; DB 1; Length 763;
Pred. No. 1.2;
4; Mismatches 26; Indels
                                                                                                                                                                                                        (BY
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(BY
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-> G (IN REF. 1).
-> P (IN REF. 1).
7C3A52A3CBBO4FB5 CRC64;
                                                                                                                                                                                                          PHOSPHORYLATION (AUTO-)
                                                                                                                                                                                                                                                                                                     MISSING (IN ISOFORM 4).
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                                                                                                                                     PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
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-> S (IN
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                                 Interpro; IPR00219; Euk_pkinase.
Interpro; IPR002290; Ser_thr_pkinase.
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33.3%;
  EMBL, AF108830; AAD31169.1;
HSSP; Q00534; 1B18.
Genew; HGNC:3091; DYRK1A.
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763 AA;
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                                                                                                                                                                                                                                                                                                                              681
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Q61214;
                                                                                                                Polymorphism.
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                     Genew; HGNC:
MIM; 600855;
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CONFLICT
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CONFLICT
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MOD_RES
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseé(isb-sib.ch).
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PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_ST; 1.
Transferase; Serine/threonine-protein kinase; Tyrosine-protein kinase; ATP-binding; Nuclear protein; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION, AND SUBUNIT.

SUBCLINE=97224401; PubMed=9070862;

SONG W.J., Chung S.H., Kurnit D.N.M.;

SONG W.J., Chung S.H., Kurnit D.N.M.;

"The murine Dyrk protein maps to chromosome 16, localizes to the nucleus, and can form multimers.";

Blochem. Blophys. Res. Commun. 231:640-644(1997).

Blochem. Blophys. Res. Commun. 231:640-644(1997).

HOUSTION: MAY PLAY A ROLE IN A SIGNALING PATHWAY REGULATING FOR IN NUCLEAR FUNCTIONS OF CELL. PROLIFERARATION. PHOSPHORYLATES SERINES, THREONINES AND TYROSINES RESIDUES IN ITS SEQUENCE AND IN EXOGENOUS
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PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-Swiss Webster / NIH;
MEDLINE-971315112; PubMed=8975710;
Song W.J., Sternberg L.R., Kasten-Sportes C., van Keuren M.L.,
Chung S.H., Slack A.C., Miller D.E., Glover T.W., Chiang P.W., Lou L.,
Kurnit D.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Isolation of human and murine homologues of the Drosophila minibrain gene: human homologue maps to 21q22.2 in the Down syndrome 'critical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phosphorylation.
BIPARTITE NUCLEAR LOCALIZATION SIGNAL
(EC 2.7.1.-) (Protein Kinase minibrain homolog) (MNBH) (MP86) (Dual specificity YAK1-related kinase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- SUBCELLULAR LOCATION: Nuclear.
-1- PTM: AUTOPHOSPHORYLATED ON TYR RESIDUES (BY SIMILARITY).
-1- SIMILARITY: BELOGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
MNB/DYRK SUBFAMILY.
                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 763;
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
POLY BER.
POLY HIS.
POLY HIS.
SER/THR-RICH.
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Pred. No. 1.2;
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InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPRU042...
InterPro; IPRU042...
Pfam; PF000069; Pkinase; 1.
ProDom; PD000001; Euk_pkinase; 1.
PMART; SM00220; S_TKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85494 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomics 38:331-339(1996).
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763 AA;
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                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration the Ewen the Swiss Institute of Bloinformatics and the EWEL outstation the Burdean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                               11 SEEVRSVAPAGFGRHGG-----GVQQHVVKEKFEEVDTVSRA------GANHHHHG 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence characteristics, subcellular localization, and substrate specificity of DYRK-related kinases, a novel family of dual specificity protein kinases."

J. Biol. Chem. 273:25893-25902(1998).

-I. FUNCTION: MAY PLAY A ROLE IN A SIGNALING PATHWAY REGULATING NUCLEAR FUNCTIONS OF CELL PROLIFERARATION. PHOSPHORYLATES SERINES, THREONINES AND TYROSINES RESIDUES IN ITS SEQUENCE AND IN EXOGENOUS
                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Dual-specificity tyrosine-phosphorylation regulated kinase 1A
(EC 2.7.1.-) (Protein Kinase minibrain homolog) (MNBH) (RPB6) (Dual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- SUBCELLULAR LOCATION: Nuclear.
-1- ALTERNATIVE PRODUCTS: 2 ISOFORNS; A LONG FORM (SHOWN HERE) AND SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
-1- TISSUE SPECIFICITY: UBIQUITOUS.
-1- PTM: AUTOPHOSPHORYLATED ON TYR RESIDUES (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND MUTAGENESIS OF TYR-219.
TRAIN-Sprague-Dawley; TISSUE-Brain;
MEDLINE-96216443; PubMed-8631952;
Rentrup H., Becker W., Heukelbach J., Wilmes A., Schuermann A.,
Huppertz C., Kainulainen H., Joost H.-G.;
"Dyrk, a dual specificity protein kinase with unique structural
features whose activity is dependent on tyrosine residues between
Subdomains VII and VIII.";
J. Biol. Chem. 271:3488-3495(1996).
                          14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-98421512; Pubmed-9748265;
Becker W., Weber Y., Wetzel K., Elrmbter K., Tejedor F.J.,
Joost H.-G.;
                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kentrup H.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                        763 AA.
                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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                                                                                                                                                                                      57 HHGGHG 62
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22;
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      Matches
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DYRA_RARA
TO 0634
DYRA_RARA
TO 0634
DYRA_RARA
DYRA 0634
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 SEEVRSVAPAGFGRHGG-----GVQQHVVKEKFEEVDTVSRA------GANHHHHHG 56
              Probom, PD000001; PALIDSSE, 1.

PRODOM, PD000001; PLW_pkinase; 1.

SMART; SM00220; S_TKC; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS550011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS550011; PROTEIN_KINASE_DOM; 1.

Transferase; Serine/threonin-proctein kinase; Tyrosine-protein kinase; ATP-binding; Nuclear protein; Phosphorylation; Alternative splicing.

DOMAIN 117 134 BIPARTITE NUCLEAR LOCALIZATION SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chesi M., Bergasgel P.L., Shonukan O.O., Martelli M.L., Brents L.A., Chen T., Schrock E., Ried T., Kuehl W.M.; Chen T., Schrock E., Ried T., Kuehl W.M.; Chen T., Schrock E., Ried T., Kuehl W.M.; Chenceden Chen T., Schrock E., Ried T., Kuehl W.M.; Chenceden E. 16q23 by Erequent dysregulation of the C-ma for Drock in multiple myeloma."; Blood 91:4457-4463(1998).

-1. SUBCELLULAR LOCATION: Nuclear (By similarity).

-1. ALTERNATIVE PRODUCTS: 2 isoforms; a long form (shown here) and a short form; are produced by alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- DISEASE: Some forms of multiple myeloma (MM) tumors are characterized by a chromosomal translocation t(14:16)(q32.3;q23)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ĕ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Euteleostom1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHOSPHORYLATION (AUTO-).
MISSING (IN SHORT ISOFORM).
Y->F: REDUCED AUTOPHOSPHORYLATION
TYROSINE, BUT NO LOSS OF HISTONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1- SIMILARITY: BELONGS TO THE BZIP FAMILY. MAF SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CBSEC7EC4C1F9A47 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SER/THR-RICH.
POLY-SER.
PHOSPHORYLATION (AUTO-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AUTO-).
                                                                                                                                                                                                                                                                                            ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
POLY-SER.
POLY-HIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAR_HUMAN STANDARD; PRT; 403 AA. 07544; 09UP93; 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Transcription factor Maf (Proto-oncogene c-maf).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 77; DB 1;
Pred. No. 1.2;
1; Mismatches 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE-98282186; Pubmed-9616139;
                                                                                                                                                                                                                                                                           PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                   POLY-HIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              that involves MAF and an 19H locus
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4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.1%;
33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22; Conservative
Pfam; PF00069; pkinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
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                                                                                                                                                                                                                                                                1159
1165
1188
2287
509
607
605
605
604
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70
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                                                                                                                                                                                                                                                                                                                                            ACT_SITE
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOD_RES
MOD_RES
VARSPLIC
MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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NP_BIND
BINDING
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DOMAIN
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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TO MAF_HUMAN

AC 07544

DT 15-JU

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alkema M.J., Jacobs J., Voncken J.W., Jenkins N.A., Copeland N.G., Satijn D.P.E., Otte A.P., Berns A., van Lohuizen M.; MPC2, a new murine homolog of the Drosophila polycomb protein is a member of the mouse polycomb transcriptional repressor complex.", J. Mol. Biol. 273:993-1003(1997).

- FUNDION: INVOLVED IN MINTAINING THE TRANSCRIPTIONALLY REPRESSIVE STATE OF GENES. MODIFIEE CHROMATIN, RENDERING IT HERITABLY CHANGED IN ITS EXPRESSIBILITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 SEEVRSVAPAGFGRHGGGVQQH-----VVKEKFEEVDTVSRAGANHHHHHHHHHGHHGGH 61
                                                                                                                                                                                                                                                                                                                                                                                                        ITEPTRKLEPSVGYATFWKPQHRVLTSVFTK -> M (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBUNIT: COMPONENT OF THE CHROMATIN-ASSOCIATED POLYCOMB COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                regulation; DNA-binding;
splicing; Chromosomal translocation.
BASIC MOTIF.
LEUCINE-ZIPPER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Chromobox protein homolog 4 (Polycomb 2 homolog) (PC2) (MPC2).
CBX4 OR PC2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 31.6%; Pred. No. 0.8;
Matches 18; Conservative 8; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              SHORT ISOFORM).
263D2FF2AF8DFB5B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 551 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- SUBCELLULAR LOCATION: Nuclear.
-i- SIMILARITY: CONTAINS 1 CHROMO DOMAIN.
                                                                                                                                                                                                                                                                                                                                                          POLY-HIS.
POLY-GLY.
POLY-GLY.
                                                                                                                                                                                                                                                                                                                                             POLY-HIS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=98035734; PubMed=9367786;
                                                                                    EMBL; AF055377; AAC27038.1; -. EMBL; AF055378; AAC27039.1; -. EMBL; AF055376; AAC27037.1; -. Genew; HGNC:6776; MAF.
                                                                                                                                                                                                                        SMART; SM00338; BRLZ; 1.
Proto-oncogene; Transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                403 AA; 41961 MW;
                                                                                                                                                                          InterPro; IPR004827; TF_bZIP.
InterPro; IPR004826; TF_Maf.
Pfam; PF03131; bZIP_Maf; 1.
                                                                                                                                                                                                                                                         Nuclear protein; Alternative
DNA_BIND 288 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                           Genew; HGNC:t
MIM; 177075;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CBX4_MOUSE
055187;
                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CBX4_MOUSE
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                                                                                                                                                                                                                       ñ
                                                                                                                                                                                                                                                                                                                                                                                                                     Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Meopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chromatin regulator; Nuclear protein; Transcription regulation;
                                                                                                                                                                                                                        .;
8
                                                                                                                                                                                             / Match 14.9%; Score 76; DB 1; Length 551; Local Similarity 37.8%; Pred. No. 1.1; hes 17; Conservative 2; Mismatches 18; Indels
                                                                                                                                                                                                                                                                      45 SRAGANHHHHHHHHGHHGGH---GFVVRETRVEEDINTCTGEVHERRE 86
                                                                                                                                              11 69 CHROMO.
383 395 POLY-HIS.
551 AA; 60581 MW; 30CEB09A82C58400 CRC64;
                                                                                                                                                                                                                                                                                                                                                                  01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
POU domain protein 1 (ZFPOUI).
                                                                                                                                                                                                                                                                                                                                            425 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; JH0710; JH0710.
HSSP; P14859; 10CT.
ZFIN; ZDB-GENE-990415-209; poul.
Interpro; IPR001356; Homeobox.
Interpro; IPR000327; POU_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proDom; PD000010; Homeobox; 1.
proDom; PD000583; POU_domain; 1.
                              MGD; MGI:1195985; Cbx4.
InterPro; IPR000953; Chromo.
Pfam; PF00385; Chromo: 1.
PRINTS; PR00504; CHROMODOMAIN.
SMART; SM00298; CHROMO, 1.
PROSITE; PS00598; CHROMO, 1.
PROSITE; PS00139; CHROMO, 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; D13045; BAA02377.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PR00028; POUDOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00046; homeobox; 1.
Pfam; PF00157; pou; 1.
     EMBL; U63387; AAB96874.1;
HSSP; P23197; 1AP0.
                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00389; HOX; 1
                                                                                                                                                                                                                                                                                                                                               POU1_BRARE
                                                                                                                                         Repressor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nterPro;
                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS;
                                                                                                                                                     DOMAIN
                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                      RESULT 12
POU1_BRARE
                                                                                                                                                                                                                    Best Loc
Matches
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CCC
DR
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KW
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SQ
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TMAF_AVIS4
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VARSPLIC
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
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                                                                                                                                                                                                                                                                                                                                                           18 APAGF---GRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHHGH-----HGGHGFVVRET 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SECUENCE OF 455-558 FROM N.A.

MEDLINE-97342649; PubMed-9199346;
Satin D.P.E., Gunster M.J., van der Vlag J., Hamer K.M., Schul W.,
Alkema M.J., Saurin A.J., Freemont P.S., van Diial R., Otte A.P.;
RINGI 1s associated with the polycomb group protein complex and acts
as a transcriptional repressor.

Mol. Cell. Biol. 17:4105-4113(1997).

-- FUNDUTION: INVOLVED IN MAINTAINING THE TRANSCRIPTIONALLY REPRESSIVE
STATE OF GERES. MODIFIES CHROMATIN, RENDERING IT HERITABLY CHANGED
IN ITS EXPRESSIBILITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Fetal brain;
MEDLINE-97459707; PubMed-9315667;
MEDLINE-97459707; PubMed-9315667;
Satijn D.P.E., Olson D.J., van der Vlag J., Hamer K.M., Lambrechts C., Masselink H., Gunster M.J., Sewalt R.G.A.B., van Driel R., Otte A.P.;
"Interference with the expression of a novel human polycomb protein, hPc2, results in cellular transformation and apoptosis.";
Mol. Cell. Biol. 17:6076-6086(1997).
                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: COMPONENT OF THE CHROMATIN-ASSOCIATED POLYCOMB COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   þe
                                                                                                         regulation; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla, Eutherla, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; may produced by alternative splicing.
-i- TISSUE SPECIFICITY: UBIQUITOUS.
                                                                                                                                                                                                                                                                                                  .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CBX4_HUMAN STANDARD; PRT; 558 AA.
000257; Q96C04;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Chromobox protein homolog 4 (Polycomb 2 homolog) (Pc2) (hPc2).
                                                                                                                                                                                                                                                        Length 425;
                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                            5C50C09CEF7EF16D CRC64;
                                                                                                                                                                                                                                                                                             33;
                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                       Pred. No. 0.95;
                                                                                                                                                                                                                                                                                           5; Mismatches
                                                                                                                                                                                                                                                 14.8%; Score 75.5; 30.9%; Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- SIMILARITY: CONTAINS 1 CHROMO DOMAIN.
                            PROSITE; PS00035; FUL,; PROSITE; PS00465; POU_2; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
Homeobox; DNA-binding; Transcription 1
84 98 ALA-RICH
                                                                                                                                                 HIS-RICH.
                                                                                                                                                                                        HOMEOBOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- SUBCELLULAR LOCATION: Nuclear
             PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS00035; POU_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                            45626 MW;
                                                                                                                                                                                                                                                                 Local Similarity 30.9
nes 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            235 HSDEDTPT 242
                                                                                                                                                                                                                                                                                                                                                                                                                    RVEEDINT 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                        425 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Colon
                                                                                                                                                                                                                                                                                                                                                                                                                    69
                                                                                                                                                                                      DNA_BIND
                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CBX4_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
SFFFF
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Avian musculoaponeurotic fibrosarcoma virus AS42.
Viruses; Retroid viruses; Retroviridae; Avian type C retroviruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-90046665; PubMed-2554284;
Mishlzawa M., Kataoka K., Goto N., Fujiwara K.T., Kawai S.;
"v-maf, a viral oncogene that encodes a 'leucine zipper' motif.";
Proc. Natl. Acad. Scl. U.S.A. 86:7711-7715(1989).
-! FUNCTION: MIGHT BE A TRANSCRIPTIONAL TRANS-ACTIVATOR.
-! SUBCELLULAR LOCATION: Nuclear.
-! DISEASE: INDUCES MUSCULOADONEUROTIC FIBROSARCOMA IN CHICKENS.
-!- MISCELLANBOUS: THIS PROTEIN IS SYNTHESIZED AS A ENV-MAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00599; CHROMO_1; 1.
PROSITE; PS50013; CHROMO_2; 1.
Chromatin regulator; Nuclear protein; Transcription regulation;
Repressor; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 75.5; DB 1; Length 558; Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: BELONGS TO THE BZIP FAMILY. MAF SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7158526991D33463 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MISSING (IN ISOFORM 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -> P (IN REF. 2).
-> C (IN REF. 2).
-> T (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50 NHHHHHHHHGHHGGHGFVVRETRVEEDINTCTGEVHERRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   369 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 1.3;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLY-HIS.
POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHROMO
                                                                                                                                                                               EMBL; AF013956; AAB80718.1; -. EMBL; BC014967; AAH14967.1; -. EMBL; U94344; AAB62734.1; -.
                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000953; Chromo.
Pfam; PF00385; chromo; 1.
PRINTS; PR00504; CHROMODOMAIN.
SMART; SM00298; CHROMO; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61228 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M26769; AAA42377.1; +. PIR; B33975; TVFVAF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 37.8 Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transforming protein Maf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                            HSSP; P23197; 1AP0.
Genew; HGNC:1554; CBX4.
MIM; 603079; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 558 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=11873;
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Search completed: June 6, 2003, 12:50:40 Job time : 14 secs
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RA Adams W.D., Celniker S.E., Holf R.A, Evans C.A., Gocayne J.D.,
RA Adams W.D., Celniker S.E., Holf W., Hoskins R.A., Galle R.F.,
RA Gocayer S.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandall M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Bazer E.G., Hell G., Nelson C.R., Miklos G.L.G.,
RA Mar K.H., Doyle C., Bazer E.G., Hell G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Barman B.P., Bhannkoch C., Basley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
Rotkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Cherry J.M., Cawley S., Dawlnec C., Davenport L.B., Davis S.P.,
RA Cherry J.M., Cawley S., Davis A.D., Dew I., Dietz S.M.,
RA Cherry J.M., Cawley S., Davis A.D., Dew I., Dietz S.M.,
RA Posler C., Gabriellan A.E., Gargn N.S., Gelbart W.M., Glasser K.,
RA Horsin D., Houston K.A., Howland T.J., Hernisa M., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wel M.-H., Ibegwam C.,
Alalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Laako P., Lei Y., Levattsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Laako P., Lei Y., Levattsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., Lidey D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., Libeyson D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wright T.R., O'Donnell J.M.;
"The catecholamines up (Catsup) protein of Drosophila melanogaster
"The catecholamines as the regulator of tyrosine hydroxylase activity.";
Genetics 153:361-382(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                             Oncogene; Transcription regulation; DNA-binding; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-99403013; PubMed-10471719;
Stathakis D.G., Burton D.Y., McIvor W.E., Krishnakumar S.,
Wright T.R., O'Donnell J.M.;
                                                                                                                                                                                                                                                                                                                                                                                      Score 75; DB 1; Length 369;
Pred. No. 0.93;
2; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 GGSVPAEEMGSAAAVVSAVIAAAAAQGGAPHYHHHHHHHHHHHHGGG 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 GGGVQQHVVKEKFEEVDTVSRAGA-----NHHHHHHHHHHGHHGGHG 62
                                                                                                                                                                                                                                                                                    BASIC MOTIF.
LEUCINE-ZIPPER.
F386B220ACE50FF6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Catecholamines up protein.
                                                                                                                                                                                                             POLY-GLY.
POLY-GLY.
POLY-GLY.
                                                                                                                                                         POLY-ALA.
HIS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-Berkeley;
MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                                                                                                                                                                                                          38892 MW;
          TRANSFAC; TUL440; TITGEPEO; INTERPRO; IPR004826; TF_MAF.
INTERPRO; IPR004827; TF_BZIP.
Pfam; PF03131; BZIP_MAF; I.
SMART; SM00338; BRLZ; I.
                                                                                                                                                                                                                                                                                                                                                                                      Query Match 14.7%;
Best Local Similarity 37.8%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                            369 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Muscomorpha; Eph
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CSUP_DROME Q9V3A4;
                                                                                                                                                                                                                                        DOMAIN
DOMAIN
DNA_BIND
DOMAIN
                                                                                                                                                              DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CSUP_DROME
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Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.K., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.W.,
Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Ra palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Käamos I., Simpson M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Tarpeleton M., Strong R., Sun E.,
Spier E., Spradling A.C., Turner R., Venter E., Wang A.H., Wang X.,
Nang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Milliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Welliams S.M., Worser I., Shong W., Zhou X., Zha S., Yao Q., Zheng Y.H., Zhong F.N., Zhong W., Zhou X., Zha S., Yao Q., Zheng Y.H., Zhong F.N., Rubin G.M., Venter J.C.;
A Glubbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
Science 287:2185-2195(2000).
C. I- FUNCTION: NEGATIVELY REGULATES TYROSINE HYDROXYLASE ACTIVITY.
C. I- FUNCTION: NEGATIVELY REGULATES TYROSINE HYDROXYLASE ACTIVITY.
C. I- SUMILARITY: BELONGS TO THE KE4/CATSUP FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                between the Swiss Institute of Bioinformatics and the EMBL outstati
the European Bioinformatics Institute. There are no restrictions on
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modified and this statement is not removed. Usage by and for commer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48 GANH-HHHHGH-----HGGHGFVVRETRVEEDINTCTGEVHERRESFLARA 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 74; DB 1; Length 449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20;
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7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (or send an email to license@isb-sib.ch)
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InterPro; IPR002395; Kininogen.
InterPro; IPR003689; Zn_trnprt_zip.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF216584; AAF37226.1; -. EMBL; AE003661; AAF53744.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48658 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 32.7
Matches 18, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                395
316
449 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF02535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transmembrane
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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Q20691 caenorhabdi
Q20699 mus musculu
Q42448 medicago sa
Q91648 strongyloce
G94441 drosophila
Q95712 medicago sa
G00116 homo sapien
Q94189 oryza sativ
Q94189 oryza sativ
Q94189 oryza sativ
G94189 oryza sativ
G94180 oryza sativ
G94180 drosophila
G944fi drosophila
Q814fi drosophila
Q814fi drosophila
Q84tj drosophila
Q94tj drosophila
      091f59 arabidopsia
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                                                                                                                                                                                                                                                                                                                                                                                                              O9kg54 bacillus | O95rh4 drosophila
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC clone:P0470A12."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 58.1%; Pred. No. 4.9e-23;
Matches 54; Conservative 14; Mismatches 21; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AP003436; BAB90280.1; -.
SEQUENCE 229 AA; 25296 MW; D6ED4AA65FFEF61E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
P0470A12.5 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  229 AA
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 QQLF59
Q20691
QQ20691
QQ30684
QQ90684
QQ90684
QQ90150
QQ104F0
QQ104F1
QQ904F1
QQ90187
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Q8S0B1;
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 RESULT
Q9SM40
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Q9sm40 sporobolus
Q8s0b2 oryza sativ
Q92xe6 arabidopsis
Q9w63 arabidopsis
Q4443 arabidopsis
Q9p543 neurospora
Q8y219 homo sativ
Q9y219 homo sativ
Q9y219 arabidopsis
Q9447 arabidopsis
Q9x342 arabidopsis
Q9x342 drosophija
                                                                                  June 6, 2003, 12:47:53 ; Search time 50 Seconds (without alignments) 383.248 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     090wv0 petromyzon
09nes7 caenorhabd1
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                                                                                                                                                             510
1 MAYYQEVDXCSEEVRSVAPA.....INTCTGEVHERRESFLARAN 93
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                                                                                                                                                                                                                                                                                           671580
   GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                   671580 seqs, 206047115 residues
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                                                         protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Q8SOB2
Q93ZA6
Q9SW63
Q24643
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Q8S0B4
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Gapop 10.0 , Gapext 0.5
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09F233
09W3D2
09VWM5
090WV0
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09Y2L9
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sp_invertebrate:*
sp_mammal:*
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sp_vertebrate:*
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sp_phage:*
sp_plant:*
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sp_bacteria:*
sp_fung1:*
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Maximum DB seq length: 200000000
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Query
Match Length DB
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18.1
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
Putative glycine-rich protein.
Sporobblus stapfianus (Ressurection grass).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Chloridoideae; Eragrostideae; Sporobolus.
                                                                                                                                                                                                                                                                                              3 YYQEVDYCSEEVRSVAPAGFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHHHHHHHGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                              Neale A.D., Blomstedt C.K., Bronson P., Le T.N., Guthridge K., Evans J., Gaff D.F., Hamill J.D.;

Evans J., Gaff D.F., Hamill J.D.;

"The isolation of lowly-transcribed genes which are induced during dessication of the resurrection grass Sporobolus stapfianus.";

Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ242802; CAB61838.1;

EMBL; AJ242802; CAB61888.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 27.6%; Score 141; DB 10; Length 102; Local Similarity 45.8%; Pred. No. 2e-08; nes 27; Conservative 8; Mismatches 18; Indels
                                                                                                                                                                                                                                       Score 177; DB 10; Length 95; Pred. No. 1.5e-12; B; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone:P0470A12.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AP003436; BAB90279.1; -
SEQUENCE 102 AA; 11214 MW; 6FF1266B1CDE7768 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Last sequence update)
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    95 AA.
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                           Created)
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1 Similarity 57.7%;
45; Conservative
                            (TrEMBLrel. 13,
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       PRELIMINARY;
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Best Local Similarity
Matches 45; Conserva
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                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                   NCBI_TaxID=56623;
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0932A6;
01-DEC-2001
01-DEC-2001
                           01-MAY-2000
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21 GFGRHGGG-VQQHVVKEKFEE----VDTVSRAGA---NHHHHHGH-HGGHGFVVRET--R 69
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Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TINY-like protein.
C7Al0.460 OR A14636900.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                              Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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Bevan M., Terryn N., Vos P., Heijnen L., Mewes H.W., Mayer K.F.X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11;
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; 299707; CAB16766.1; -.
EMBL; AL161590; CAB80356.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yamenuzu - . . . Ecker J.R.;
Ecker J.R.;
"Arabidopsis cDNA clones.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AX057683; AAL15314.1;
InterPro; PR0001471; TF_ERF.
Pfam; PF00847; AP2-domain; 1.
Probom; P0001423; TF_AP2; 1.
Probom; P001423; TF_AP2; 1.
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Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18.1%; Score 92.5; DB 10;
33.8%; Pred. No. 0.013;
iive 12; Mismatches 24;
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Interpro; IPR001471; TF_ERF.
Pfam; PR00847; AP2-domain; 1.
PRINTS; PR00367; ETHRSPELEMNT.
ProDom; PD001423; TF_AP2; 1.
SMART; SM00380; AP2; 1.
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Best Local Similarity 33.8%
Matches 24; Conservative
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159 INDDLMECSSK 169
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Related to multifunctional cyclin-dependent kinase PHO85 B24H17.10.
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InterPro; IPR004129; GDPD.
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Best Local Similarity 72.2
Matches 13; Conservative
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Best Local Similarity 26.9%
Matches 25; Conservative
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'fam; PF03009; GDPD; 1
'fam; PF03105; SPX; 1.
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Q8S0B4
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                                                                                                                                                                                     21 GFGRHGGG-VQQHVVKEKFEE----VDTVSRAGA---NHHHHHHH-HGGHGFVVRET--R 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JAN-1998 (TrEMBLrel. 21, Last annotation update)
11NY-11ke protein (Fragment).
11NY-11ke protein (Rouse-ear cress).
12NY-11ke protein (Mouse-ear cress).
12NY-11ke protein (Mouse-ea
                                                   18.1%; Score 92.5; DB 10; Length 196;
33.8%; Pred. No. 0.013;
tive 12; Mismatches 24; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Okamuro J.K., Caster B., Villarroel R., van Montagu M., Jofuku K.D.;
"The AP2 domain of APETALA2 defines a large new family of DNA binding
Proc. Natl. Acad. Sci. U.S.A. 94:7076-7081(1997).
EMBL. A7002598; CAA65630 1;
EMBL. A7003103; AAC49776.1;
HSSP; 080337; 2GCC.
Interpro; INTERPRO! ITP_ERF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18.1%; Score 92.5; DB 10; Length 259; 33.8%; Pred. No. 0.018; Live 12; Mismatches 24; Indels 11
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     21362 MW: 0023D5571345C6A0 CRC64;
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259 AA; 28615 MW; 0464949DB6C619DB CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00847; AP2-domain; 1.
PRINTS; PR00367; ETHRSPELEMNT
ProDom; PD001423; TF_AP2; 1.
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(TrEMBLrel. 15, I
(TrEMBLrel. 21, I
                                                                                                      Conservative
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159 INDDLMECSSK 169
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        AA;
                                                                              Local Similarity
les 24: Conserv
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     196
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09P543;
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01-0CT-2000 (
  SEQUENCE
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Best Local (
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SEQUENCE
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Matches 24,
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ID Q9P5.
AC Q9P5.
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DT 01-01
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12 EEVRSVAPAGFGRH----GGGVQQHVVKEKFEEVDTVSRAGA-----NHH------52
                                                                                                                                                Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R., Nyakatura G., Mewes H.W., Mannhaupt G.; Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spérmatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoldeae; Oryzeae; Oryza.
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Neurospora crassa.
Eukaryota; Fuugi, Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID-5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-CV. NIPPOWERE;
Sasaki T., Matsumoto T., Yamamoto K.;
Oryza sativa nippombare(GA3) genomic DNA, chromosome 1, PAC
Clone:P0470A12."
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AP003436; BAB90277.1; - FPE0297877F6D69C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1245;
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PROSITE; PS50297; ANK_REP_REGION; 1.
ANK_repeat; Cyclin; Kinase; Repeat.
SEQUENCE 1245 AA; 137798 MW; 16BD0F6A04596A9F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                           German Neurospora genome project;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
EMBL; ALJ56815; CAB92623.1;
HSSP; P42773; LIHB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
P0470A12.2 protein.
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259 HHYGGATAAAYGNASNKQHFTAAAAGHHSSGGH 291
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Ecker J.R.;
"Arabidopsis
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SEQUENCE
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26
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MEDILINE-94150718; bubmed-7906398;

Wilson R., Adnacrough R., Baynes C., Berks M.,

Wilson R., Adnacough R., Connell M., Copsey T., Cooper J., Coulson A.,

Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,

Jones M., Kershaw J., Kirsten J., Laister N., Latraille P.,

Lighting J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,

Persons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,

Smaldon N., Smith A., Sonnhammer E., Staden R., Sullston J.,

Thierry-Mieg J., Thomas K., Yaudin M., Vaughan K., Waterston R.,

Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;

"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                       Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases. EMBL, AF125964; AAD14753.1; -SEQUENCE 471 AA; 50885 MW; BDF30B59A64A985B CRC64;
                                                                                                                                                                                                                                                                                                                                                                              Pauley A., Scheet P., Harper M.;
"The sequence of C. elegans cosmid W03G1.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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Last annotation update)
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                                                                    Created)
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                                              PRT;
                                                   Ol-MAY-2000 (TrEMBLrel. 13, C. 01-MAY-2000 (TrEMBLrel. 13, La 01-JUN-2001 (TrEMBLrel. 17, La W03G1.5 Protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KIAA1016 protein (Fragment) KIAA1016.
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                                                PRELIMINARY;
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Nature 368:32-38(1994).
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427 PPHHGHHHF 435
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Best Local Similarity
Matches 24; Conservi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Waterston R.
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6 EVDYCSEEVRSVAPAGFGRHGGGVQQHVVKEKFEE---VDTVSRAGA-----NHHHHH 55
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Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
Cheuk R., Chen H., F., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
Bowser L., Carninci P., Dale J.M., Kamiya A., Karlin-Neumann G.,
Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Mirranda M., Narusaka M.,
Nguyen M., Onodera C.S., Palm Ç.J., Pham P.K., Quach H.L., Sakurai T.,
Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
      Nagase T., Ishikawa K., Suyama M., Kikuno R., Hirosawa M.,
Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. XIII.
The complete sequences of 100 new cDNA clones from brain which code
for large proteins in vitro.";
DNA Res. 6:63-70(1999).
EMBL; AB023233; BAA76860.1;
InterPro; IPR001114; HPL-SerP_site.
InterPro; IPR001114; HPL-SerP_site.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
At154990/F14C21_5
Arabidopsis thaliam (Mouse-ear cress).
Enkaryota: Viridiphantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta: Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF424608; AAL11602.1;
SEQUENCE 441 AA; 48816 MW; 520163FE0A8DE447 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0BE99CC48C3BB37C CRC64;
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PROSITE; PS00589; PTS_HPR_SER; UNKNOWN_1.
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MEDLINE=99246063; PubMed=10231032;
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                                                                                                                                                                                                                                                                                                            InterPro; IPR003592; LRR_out.
InterPro; IPR003591; LRR_typ.
Pfam; PF00307; CH; 1.
Pfam; PF00560; LRR; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS: PRO0019; LEURICHRPT. SMART; SM00033; CH; 1. SMART; SM00370; LRR; 3. SMART; SM00369; LRR, TYP; 1.
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Best Local Similarity 36.8%
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 16.9%
Best Local Similarity 32.8%
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99 ОНИССТС 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56 GHHGGHG 62
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409 DYISEFV-SLLPKSIRR----VAEEPIPEEVQKVLEEAKAGDDHDHHHGHGHAHAGY 460

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RESULT 13
Q9W3D2
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WEDLINE-21016719; PubMed-11130712;
WEDLINE-21016719; PubMed-11130712;
WEDLINE-21016719; PubMed-11130712;
WEDLINE-21016719; PubMed-11130712;
WHITE O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
White O., Alonso J., Altafi H., Cheuk R.F., Chin C.W.,
Chung M. K., Conn L., Conway A.B., Creasy T.H., Dewar K.,
A Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujil C.Y.,
M. Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Knan R., Hunter J.L., Jonkinson Hopson C., Khan S., Knaykin E.,
M. M. C.J., Koo H.L., Kremenetskala I., Kurtz D.B., Kwan B.,
Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
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M. M. Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
Sakano H., Zallon L.J., Tambunga G., Torlumi M.J., Town C.D.,
Why Tallon L.J., Tambunga G., Torlumi M.J., Town C.D.,
Wellerback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
Sequence and analysis of chromosome I of the plant Arabidopsis
377 DYISEFV-SLLPKSIRR----VAEEPIPEEVQKVLEEAKAGDDHDHHHGHGHAHAGY 428
                                                                                                                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
101-MAR-2002 (TrEMBLrel. 20, Last annotation update)
124C10.10 protein (Hypothetical 52.4 kDa protein).
174C10.10 or F14C2.15.10 R ATIG54990.
174Ac10.10 or F14C2.15.10 R ATIG54990.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicctyledons; core eudicots; Rosidae; NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen.N.F., Altafi H., Nguyen M., Lam B., Southwick A., Miranda M., Brooks S., Buehler E., Chao O., Chin C., Chiou J., Choi E., Gonzalez A., Lenz C., Liu A., Liu S., Mukharsky N., Pham P., Sakano H., Shinn P., Toriumi M., Vaysberg M., Yu G., Ecker J., Theologis A., Davis R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M., Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J., Sakiwai J., Sakim Y., Sakim W., Seki M., Shinn P., Southwick A., Shinozaki K., Full Length cDNs of gene Arigidago (GI:15221965)."

Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 protein.
473 AA: 52419 MW; D09124A11565BB23 CRC64;
                                                                                                                                                                                          473 AA.
                                                                                                                                                                                       PRT;
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                                                                                                                                                                                   PRELIMINARY;
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Best Local Simi
Matches 21;
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                                                                                                        RESULT 12
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RY SEQUENCE FROM N.A.

RY SEQUENCE FROM N.A.

RAMADINE-10918606; Pubmed-10731132;

RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,

Adams M.D., Celniker S.E., Elither R.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,

Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,

RA Gorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,

RA Bardon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Barll J.F., Agbayanl A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Barll W.R.W., Basu A., Baxendall J., Baytaktarolan C.R., Millog G.L.G.,

RA Barll W.R. K.C., Buttler H., Caddeu E., Center A., Chandra I.,

RA Burtis K.C., Butam D.A., Buttler H., Caddeu E., Center A., Chandra I.,

RA Burtis K.C., Butler H., Caddeu E., Center A., Chandra I.,

RA Burtis K.C., Busam D.A., Bahlke C., Davenport L.B., Daviss P.,

RA Color E., Downes M., Dahlke C., Davenport L.B., Daviss P.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,

RA Dodson K., Cong F., Gorrell J.H., Gu Z., Gunn P., Harris M.L.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Harris M.

RA Hostin D., Houston K.A., Howland T.J., Well M.-H., Ibegwam C.,

Joldek A., Gong F., Gorrell J.H., Gu Z., Kennison J.A.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.K., Machelson D.,

RA Mount S.M., May H., Murphy B., Li Z., Liang Y., Lin X.,

RA Houth S.M., My H., Murphy B., Mortherson D.,

RA Mount S.M., My H., Murphy B., Li Z., Liang Y., Lin X.,

RA Spier E., Spradling A.C., Standers R.D.C., Scheeler F., Shelp L.,

RA Spier E., Spradling A.C., Standers R.D.C., Scheeler F., Shelp L.,

RA Spier E., Spradling A.C., Standers R.D.C., Scheeler F., Shelp L.,

RA Wanner S.M., Woy H., Wurphy B., Worley S., Yon G., Zheo Q., Zheng L.,

RA Wanner S.M., Wodage T., Worley K.C., Wu D., Yang S., Zhu X., Salth H.O.,

RA J. Yeh R. F., Zavori J.S., Zhan M., Zhong S., Zha X., Zhan R., Shence C., Shence C., 
                                                                                                                            Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 16.5%; Score 84; DB 5; Length 1561; I Similarity 23.9%; Pred. No. 1.4; 28; Conservative 17; Mismatches 30; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1561 AA; 174616 MW; 10BFD38A3DD4FC4E CRC64;
                                     (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
  PRT; 1561 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE003444; AAF46397.1;
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InterPro; IPR005112; dDENN.
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  PRELIMINARY;
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fam; PF02141; DENN; 1.
fam; PF03456; uDENN; 1.
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SEQUENCE FROM N.A.
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Matches 28; Conserv
                                                                                                      CRAG protein.
CRAG OR CG12737.
                                     01-MAY-2000
                                                         01-MAY-2000
01-JUN-2002
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09W3D2
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8; Gaps

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DYCSEEVRSVAPAGFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHHGH----HGGH 61

Conservative

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Celniker
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
A Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
A Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
A George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
B Sutton G.G., Wortman H.R., Yandall M.D., Zhang Q., Chen L.X.,
A Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Basu A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Barman B.P., Bhardari D., Beasley E.M.,
Ballew R.M., Cawley S., Lablike C., Davenport L.B., Davies P.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
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A Burtis K.C., Busam D.A., Bulle C., Davenport L.B., Davies P.,
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A Harris N.L., Harvey D., Helman T.J., Herriande J.R., Houck J.,
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A Laako P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
A Laako P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
A Raharian R., Moy M., Murphy B., Murphy L., Muzny D., Puri V., Reese M.G.,
A Raharzollo M., Pittman G.S., Pollard J., Puri V., Reese M.G.,
A Spier E., Spradling A.C., Stepleton M., Strong R., Yano S., Yao O.A.,
A Wariskas R., Tector C., Turner E., Wang A.H., Wang Z., Yu.
                                   12 EEVRSVAPAGFGRHGGGVQQ-----HVVKEKFEEVDTVSRA------47
                                                                                                                                                             Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zhong X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O. Gibbs R.A., Wyers E.W., Rubin G.M., Venter J.C., "The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                         48 GANH-----HHHHGHHGGHGFVVRE------TRVEEDINTCTGEVHERRES 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., Gorgel R., Gonzallez M., Guaralin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                       U1-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequ
01-UNN-2002 (TEMBLrel. 21, Last anno
CG7406 protein (RE04580p).
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                                                                                                                                                                                                                                                                                          RESULT 14
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3 YYQEVDYCSEEVRS---VAPAGFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHHGHHG 59
                                                                                                                                                                                                                                                        46 VKVISEE-----AGHGGWAGGYSGGYAH-APEEVKIVKVISEAGHSHGHDYGHSHGHGS 98
                                                                                                                                                                                                                                  7 VDYCSEEVRSVAPPAGFGRHGGGVQ---QHVVKEKFEEVDTVSRAGANHHHHHHHHGHHGGHGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Petromyzon marinus (Sea lamprey).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Petromyzon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Force A., Amores A., Postlethwait J.;
"Hox cluster organization in the jawless vertebrate, Petromyzon marinus, and the evolution of the vertebrate Hox clusters.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, ANDS469; AAL17914.1;
InterPro; IPR001825; Antennapedia.
InterPro; IPR001825; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3;
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                                                                                                                                       16.3%; Score 83; DB 5; Length 168; 32.9%; Pred. No. 0.13;
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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE003511; AAF48913.1; -.
EMBL; AX089569; AAL90307.1; -.
FlyBase; FBgn0030980; CG7406.
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                                                                                           168 AA; 16791 MW; B14DF461A0AB0F40 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16.2%; Score 82.5; DB 13;
29.0%; Pred. No. 0.38;
Live 9; Mismatches 32;
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                                                                                                                                                                                        9; Mismatches
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PROSITE; PS00032; ANTENNAREDIA; UNKNOWN_1.
PROSITE; PS00027; HOMEOBOX_1; UNKNOWN_1.
PROSITE; PS50071; HOMEOBOX_2; 1.
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                                                                                                                                                 Query Match 16.3
Best Local Similarity 32.9
Matches 26; Conservative
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Job time: 52 secs
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

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Command line parameters:

WODEL_frame+_p2n.model -DEV-x1h
-0-7gn2_1VSFV0_spool_VSI0090035/runat_06062003_105504_10970/app_query.fasta_1.526
-0.7gn2_1VSFV0_spool_VSI0090035/runat_06062003_105504_10970/app_query.fasta_1.526
-0.0B-EST -0.FWT=fastap -SUFFIX=rst -WINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-0.0VTRT-0.00 -TRR_SCORE-pct -THR_MAX=100 -THR_WIN-0 -ALIGN-15 -MODE-LOCAL
-0.0TFRT-pto -NORM-ext -HEAPSIZE-500 -MINNEN-200000000
-0.0TFRT-0.00 -THR_SCORE-pct -THR_WIN-0 -MAXEN-200000000
-0.0TFRT-0.00 -MORP -LARGEQUERY -NEG_SCORES-0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT-120 -WARR_TIMEOUT-30 -THREADS-1 -XGAPOP=10 -XGAPEXT-0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT-0.5 -DELOP=6 -DELEXT-7
                                                        % Search time 1293.5 Seconds
(without alignments)
1164.422 Million cell updates/sec
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510
1 MAYYQEVDYCSEEVRSVAPA.....INTCTGEVHERRESFLARAN 93
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OM protein – nucleic search, using frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
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7.0
                                                        June 16, 2003, 10:02:07
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Perfect score:
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em\_gss\_other:\* em\_gss\_pro:\* em\_gss\_rod:\* em\_esthum:\* em\_estin:\* em\_estmu:\* em\_gss\_hum:1 em\_gss\_inv:\* em\_gss\_pln: em\_gss\_fun:\* ет\_дзѕ\_тат:\* em\_gss\_mus:\* em\_estfun:\* em\_estom:\* gb\_gss:\* em\_estpl:\* em\_estro:\* gb\_est3:\*
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gb\_est5:\* em\_estba:\* em\_estov: \* gb\_estl:\* gb\_est2 em\_htc;\* gb\_htc: EST: \* 10: 11: 12: 13: Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

7	יייייייייייייייייייייייייייייייייייייי	BM501439 PAC00000	BE12969/ 945032C12	AM/6//52 943002EU6	AW288876 707009504	A1964534 496013001	AI964458 496010H04	AI855425 603016F02	AA979839 MEST2-B7.	BG840383 MEST12-H1	ALICATOS SEG MAYS ROFIGIAL BNOSEOAFO	BO619315 RNOSEOGCO	BQ619318 RNOSEO6D0	BQ619337 RNOSEQ6E1	BQ619383 RNOSEQ7B0	BQ619390 RNOSEQ7B0	BEU233U3 943U28BU9	BE025302 94502800	BE519299 945007B05	AW787314 945002E06	BE225008 945042F02	AW787315 945002E06	BM3186/2 PII_I6_CO	BE599123 PI1 R5 F0	BQ280709 WHE3004_A	BE364814 PII_16_C0	AW680016 WS1_34_H1	AW745400 WS1 34 H1	AW745436 WS1_34_B0	BE593507 WS1_100_B	BU280894 WHE3006_B	AW288875 707009E07	BF729420 1000077C0	AW923922 WS1_30_A1	AW679915 WS1_33_G0	AW577017 12 10 00	AW746383 WS1 49 G0	AW679713 WS1_30_A1	AW925014 WS1_74_D0	TS		ANG TOTAL TOTAL					ophyta; Embryophyta; Tracheophyta; liopsida; Poales; Poaceae; PACC	z; zea.	Y,G., Hamaker,B., Larkins,B.A. and
Ę						AI964534	AI964458	AI855425																														AW679713		ALIGNMENT		7	er AF-1 array	13			; Strept hyta; Li	iat opogoneae	., Singletary
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& Query Match		99.0	99.0	99.0	0.66	97.9	97.9	97.9	0.70	97.9	97.9	97.9	97.9	y	6.70	97.6	97.3	97.3	96.9	36.5	. a	83.0	83.0	83.0	83.0	0.0	83.0	83.0	83.0	80 T	77.5	72.3	72.1	9.09	60.4	60.4	60.4	60.4 60.4				1439	0000000	BM501439.1	mays	mays	Spermatophyta; clade: Panicoi	(bases 1	er, B.G. , R.
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945032C12.X1 945 - Mixed adult tissues from Walbot lab, same as 707 (SK) Zea mays cDNA, mRNA sequence.
BE129897.1 GI:8577260
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Walbot,V.
Maize ESTs from various cDNA libraries sequenced at Stanford
                                                                                                                                       /organism="Zea mays"
/db_xref="taxon:4577"
/clone_llb="Pioneer AF-1 array"
/clone_vector: psportl; Site_1: Sall; Site_2: NotI"
/clone_vector: psportl; Site_1 = 33 f
    무
Maize opaque endosperm mutations create extensive changes patterns of gene expression Unpublished (2002)
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Contact: Walbot V
Department of Biological Sciences
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AW787732
945002E06.X3 945 - Mixed adult tissues from Walbot lab, same as 707
(SK) Zea mays cDNA, mRNA sequence.
AW787732.1 GI:7844510
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/cote="Organ: tassel, ste_l: EcoRI; cDNA library from fully
differentiated maize tissues from an active Mutator plant.
Tissue ratio is 4:2:1:1:1:1 (tassel, kernel, silk, husk,
root, leaf). Unidirectionally cloned. New library number
given to library 707 for additional sequencing."
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                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:4577"
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/clone_lib="945 - Mixed adult tissues from Walbot lab, same as 707 (SK)"
/tissue_type="tassel, kernal, silk, husk, root, leaf"
/dev_stage="fully-grown"
/lab_host="DH10B"
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855 California Ave, Palo Alto, CA 94304, USA
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Contact: Walbot V
Department of Biological Sciences
Email: walbot@stanford.edu
Plate: 945032 row: C column: 12.
Location/Qualifiers
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                                                    /organism="Zea mays"
                                                                 /cultivar="W23"
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/organism="Zea mays"
/cultivar="W33"
/db_xref="taxon:457"
/clone_lib="945 - Mixed adult tissues from Walbot lab,
same as 707 (SK)"
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/lab_host="pully-grown"
/lab_host="pully-grown"
/lab_host="pully-grown"
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/note="Corgan: tasse! kernal, silk, husk, root, leaf;
Unidirectionally cloned. New library number
given to library 707 for additional sequencing."
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tissues from Walbot lab (SK) Zea
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1 (bases 1 to 523)
Walbot,V.
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Matches:
Conservative:
Mismatches:
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 945002 row: E column: 06.
Location/Qualifiers
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Contact: Walbot V
Department of Biological Sciences
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/dev_stage="adult"
/lab_host="nglis"
/note="Organ: tasse; kernel, silk, husk, root, leaf;
/note="Organ: tasse; kernel, silk, husk, root, leaf;
/ector: pGAD10; site_1: ECORI: cDNA library from fully
vector: pGAD10; site_1: ECORI: cDNA library from fully
plant. Tissue ratio is 4/2/1/1/1/1 (tassel, kernel, silk,
husk, root, leaf): undirectionally cloned."
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1 (bases 1 to 524)
Walbot,V.
Walbot,V.
Malze Esrs from various cDNA libraries sequenced at Stanford Unpublished (1999)
Contact: Walbot V
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                                                                                                                  1. .523
/organism="zea mays"
/oultiva="W13" ways"
/db_xref="taxon:4577"
/clone_lib="707 - Mixed adult tissues from Walbot lab
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Stanford University
855 California Ave, Palo Alto, CP
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 707049 row: E column: 0/
Location/Qualifiers
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707009E07.x4 707 - Mixed adult the mays cDNA, mRNA sequence.
AW288876.1 GI:6695663
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoldeae; Andropogoneae; Zea.
1 (bases 1 to 466)
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/dev_stage="adult"
/lab_host="nbll0B"
/note="organ: tassel, kernel, silk, husk, root, leaf;
/note="organ: tassel, kernel, cDNA library from fully
vector: pGADIO; Site_1: EcoRI; cDNA library from fully
fulferentiated maize tissues from an active Mutator
plant. Tissue ratio is 4/2/1/1/1/1 (tassel, kernel, silk,
husk, root, leaf). Gnidirectionally cloned."

a 170 c 157 g 89 t lothers
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              Stanford University
855 California Ave, Palo Alto, CA 94304, USA
7E1: 650 723 2227
TEX: 650 725 8221
Email: walbot@stanford.edu
Plate: 707009 row: E column: 07.
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Conservative:
Mismatches:
Indels:
Gaps:
    Department of Biological Sciences
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Maize ESTs from various
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Unpublished (1999)
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AI964534.1 GI:5757247
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A1964458 481 bp mRNA linear EST 20-AUG-1999 496010H04.x1 496 - stressed shoot cDNA library from Wang/Bohnert Llab Zea mays cDNA, mRNA sequence.
A1964458 A1964458.1 G1:5757171
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
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Walbot,V.
Maize ESTs from various cDNA libraries sequenced at Stanford
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/db_xref="taxon:457"
/clone_lib="496 - stressed shoot cDNA library from Wang/Bohnert lab"
/tissue_type="seedling"
/dev_stage="salt stress"
/dab_host="E.coli XL Gold"
/note="corgan: shoot; Vector: pBluescriptII SK(+) XR;
/note="corgan: shoot; Wector: pBluescriptII SK(+) XR;
/note="corgan: shoot; W
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Department of Biological Sciences Stanford University Palo Alto, CA 94304, US; R55 California Ave, Palo Alto, CA 94304, US; Fax: 650 723 2227
Fax: 650 725 8221
Email: walbottetenford.edu
Plate: 496013 row: D column: 01.
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Department of Biological Sciences
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                                                                                                                                                                                                                                                                                                                                                /organism="Zea mays"
/cultivar="B73"
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us-10-090-035-2.rst

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A1855425 603016F02.X1 603 - stressed root cDNA library from Wang/Bohnert lab Zea mays cDNA, mRNA sequence.
A1855425. GI:5499558
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 539)
                                                                                     1. .481
/organism="Zea mays"
/organism="Zea mays"
/db_xref="1873"
/db_xref="1873"
/clone_lib="496 - stressed shoot cDNA library from
Mang/Bohnert lab"
/tissue_type="seedling"
/dev_stage="salt stress"
/lab_host="E.coli XL Gold"
/note="Jorgan: shoot; Vector: pBluescriptII SK(+) XR;
Wang/Bohnert
2 a 148 c 154 g 97 t
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Maize ESTs from various cDNA libraries sequenced at Stanford
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855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Exa: 650 725 8221
Email: walbot@stanford.edu
Plate: 496010 row: H column: 04.
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Contact: Walbot v
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
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Matches:
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Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoldeae; Andropogoneae; Zea.
1 (bases 1 to 546)
Wen,T.J., Ashlock,D.A. and Schnable,P.S.
Expressed Sequence Tags from B73 Maize Seedlings
Onpublished (1997)
Contact: Schnable, PS.
                                                                                                                                                                                                                                                                                            21 GlyPheGlyArgHisGlyGlyGlyAlGlnGlnHisValValLysGluLysPheGluGlu
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Matches:
Conservative:
Mismatches:
Indels:
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 603016 row: F column: 02.
Location/Qualifiers
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G405 Agronomy, Ames, IA 50011,
Tel: (515)-294-0975
Fax: (515)-294-2299
Email: schnable@lastate.edu
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MEST12-H11.T7-1 ISUM4-TN Zea mays cDNA clone MEST12-H11 5', mRNA
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 550)
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/tissue_type="above ground tissues"
/dev_stage="Two-leaf-stage green seedling"
/lab_host="XL1-MFR Blue"
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          PCR PRimers
FORWARD: tw1412 (5'-GAAGATACCCCACCAACC-3')
BACKWARD: T7-YJ (5'-TAATACGACTCACTATAGGC-3')
Plate: MEST2 row: B column: 7
Seq primer: tw1412 (5'-GAAGATACCCACCAAACC-3').
Location/Qualifiers
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/clone="MEST2-B7"
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Expressed Sequence Tags from B73 Maize Seedlings and Silks
Expressed Sequence Tags from B73 Maize Seedlings and Silks
Unpublished (2001)
On May 25, 2001 this sequence version replaced gi:14206705.
Contact: Patrick S. Schnable
Schnable Laboratory
I cow State University
G405 Agronomy, I owa State University, Ames, IA 50011-1010, USA
Tel: 515-294-0975
Fax: 515-294-2299
Email: schnablediastate.edu
PCR PRIMETS
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Eca mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Wagnoliophyta; Liliopaida; Poales; Poaceae; PACC

clade; Panicoldeae; Andropogoneae; Zea.

1 (bases 1 to 648)

Wang; H. and Bohnert, H.J.

Genomics of plant stress tolerance

Unpublished (2002)

Contact: Mark Fredicksen

Department of Plant Biology
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Tel: 2172655473
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Location/Qualifiers
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Zea mays
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Spermatophyta; Manoliophyta; Liliopsida; Poales; Poaceae; PACC
Clade; Panicoideae; Andropogoneae; Zea.

1 (basea I to 553)
SR Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S.,
Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
Malze Mapping Project/DuPont Consensus Sequences for Design of
Overgo Probes
IAL Unpublished (2002)
SR Coe, E.C.
Jurect Submission
Submitted (25-APR-2002) Malze Mapping Project, University of
Missouri, Columbia, MO 65211, USA
Location/Qualifiers

Location/Qualifiers
   HTC 25-MAY-2002
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RNOSEG4E05_SK.abl Salt stressed Zea mays roots cDNA library Zea
mays cDNA clone RNOSEQ4E05_SK.abl similar to No homology, mRNA
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Matches:
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  mRNA
      Zea mays PCO124784 mRNA sequence.
AY104409
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Pantcoldeae; Andropogoneae; Zea.

1 (bases 1 to 648)

25 1 (bases 1 to 648)

26 Mang, H. and Bohnert, H.J.

26 Genomics of plant stress tolerance

AL Onpulshed (2002)

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Tel: 2172655473

Email: bohnertlabellife.uiuc.edu.

Email: bohnertlabellife.uiuc.edu.

Ab xref="taxon:4577"

/clone="RNOSEO6C06_SK.abl"

/clone="RNOSEO6C06_SK.abl"

/clone="taxon:4577"

/dev_stage="2" weeks old"

/notes" weeks old"

/notes" weeks old"

/notes" Wector: pBluescript SK+; Stressed 24 hours at 150

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1 (bases I to 648)
Wang, H. and Bohnert, H.J.
Genomics of plant stress tolerance
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BQ619318
                                                                    AUTHORS
TITLE
JOURNAL
                                                        REFERENCE
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EST 27-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41 ValAspThrValSerArgAlaGlyAlaAsn---HisHisHisHisHisGlyHisHisGly 59
                                                                                                                                                                                                                                                                                                                                                                                                                                  40
                                                                                                                                                                                          at 150
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RNOSEQ6E12_SK.abl Salt stressed Zea mays roots cDNA library Zea
mays cDNA clone RNOSEQ6E12_SK.abl similar to No homology, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Zea mays"
/organism="Zea mays"
/organism="Exacon:4577"
/olone="RNOSEQ6D01_SK.abl"
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/closue_lbp="Roots"
/dev_stage="Z weeks old"
/dev_stage="Z weeks old"
/dev_stage="Z weeks old"
/dev_stage="Z weeks old"
                                                                                                                                                                                        Stressed 24 hours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    648
93
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Unpublished (2002)
Contact: Mark Fredricksen
Department of Plant Biology
University of Illinois
1201 W. Gregory Dr., Urbana, IL 61801, USA
Tel: 2172655473
                                                                                                                                                                                                                                                                                              Conservative:
Mismatches:
Indels:
                                                                                                                                                                                           /note="Vector: pBluescript SK+;
                                                                                                                                                                                                                                                                     Length:
Matches:
                                                                                                                                                                                                                   100
                                                                              Email: bohnertlab@life.uiuc.edu.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                          US-10-090-035-2 (1-93) x BQ619318 (1-648)
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BQ619337.1 GI:21621331
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1. .648
/drganian="Zea mays"
/db_xref="taxon:457"
/db_xref="taxon:457"
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/dev_stage="2 weeks old"
/note="Vector: pBluescript SK+; Stressed 24 hours at 150
mm NaCl"
                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Email: bohnertlab@life.uiuc.edu.
Location/Qualifiers
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Job time: 1303.5 secs
                                                                                                  183 9
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499.50
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Best Local Similarity:
Query Match:
DB:
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OM nucleic - nucleic search, using sw model

Run on:

June 16, 2003, 04:03:20 ; Search time 1684.8 Seconds (without alignments) 9915.101 Million cell updates/sec

Title: Perfect score: Sequence:

OLIGO\_NUC Gapop 60.0 , Gapext 60.0 Scoring table:

2054640 seqs, 14551402878 residues Searched:

0

Word size :

Total number of hits satisfying chosen parameters:

4109280

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmb1:\*

gb\_ba: \*
gb\_htg: \*
gb\_in: \*
gb\_om: \* gb\_ov:\* gb\_pat:\* gb\_ph:\* gb\_p1:\*

gb\_pr:#gb\_ro:#gb\_sts:#gb\_un:#gb\_vi:#em\_ba:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_fun:#em\_

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\_other:\* em\_htg\_pln: \* em\_htg\_rod: \* em\_htg\_mam: \* em\_htg\_hum:\* em\_htg\_inv:\* em\_htg\_mus:\*

em\_htgo\_other:\* em\_htgo\_hum:\* em\_htgo\_mus:\* em\_htg\_vrt:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

UMMARIES	
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ALIGNMENTS

RESULT 1 AP003416/c LOCUS DEFINITION

AP003416
Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, PAC clone:P0456E05.
AP003416
AP003416.4 GI:20804922 ACCESSION VERSION KEYWORDS SOURCE

Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA, clone:P0456E05.
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplanicae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryzea. ORGANISM

REFERENCE

AUTHORS TITLE

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

JOURNAL

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join(36977 . 37082,37255 . 37479,37607 . 37701,37823 . 38015,
38424 . 38764,39169 . 39399,39493 . 39645)
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RFLAATRDISVQGDLNLFPSLPYSCSLAAAGLVL"

join(18574. .18678,18821. .18984,20752. .21058,21870. .22177,
22377. .22536)

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/gene="p0456E05.3"
                                                                                         oin(18574. .18678,18821. .18984,20752. .21058,21870. .22177,
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LVVGFNCAYVLSFSNLAMAPLGWGWGTACLLFIGAAGWYANWILAGLHYIDGGREIRY
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RDLMGFYFARAYFVPTISAMKNWLATSAALTVAXDVALIVILIKDGKSNKQKDYNVH
IAATGEVYFARAYFVPTISAMKNWLATSAALTVAXDVALIVILIKDGKSNKQKDYNVH
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ISVAQYWAYGAAVSEYLPDQLSGPSWATVLINATAFLQSIVSQHLFTVPIHEALDTQM
ORLDEGMFSRYNLGRRLLARGLVFGANAFVTALFPFWGDFVNLFGSFVLFPLFFMFPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MVVLKIKGKDEAGRWNRIWHWGIIVASSVLSVVTTAAAVRLIVHNASVYHFFADM"
complement(join(40277. 40417,40717. 40773,40875. 41073,
41173. .41300,41399. .41504,41677. .41756,42145. .42242,
42324. .42437,42523. .42663,42757. .42841,43717. .44055))
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ILQRRIKKERDAAAGGGKVRRAVVLIRGVTDDAAAAFVRLITAGSSGDEBEIDEKSAA
OMLVLAHATAGSSGDEBEIDEKSAA
OMLVLAHATVPWLKRRCGAGSRICHTAESVVPMQLAALCDAPQLHIRCTRLIAKEF
RAVEKTBAMRFLQENDPWLELDILQRLHDADURRKRRRRADGGVYVELSEBAMDCLS
HICTEGCTEVGPVGRAPAAAPCPAYATACRGLQLLIRHFSRCHRTSCPRCQRWWQLLR
IHAALCDLPDGHCNTPLCMQFRRKEEEKAAARAKAKAGDDDDKWGLLVKRVRVARAMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'translation="MVKVATYFAMTFGAFLFWQSMDRVHVWIALHQDEKKERMEREQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(join(26102. .26407,26766. .26901,27028. .27170,
27656. .27784,28154. .28402,28988. .29359))
/gene="P0456E05.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(join(26102. .26407,26766. .26901,27028. .27170,
27656. .27784.28154. .28402,28988. .29359))
/gene="p0456E05.5"
                                                                                                                                                                 /note="contains EST AU070785(R10238)
similar to Arabidopsis thaliana chromosome 3, At3948360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 37701,37823.
38424. 38764,39169. 39399,39493. 39645)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(join(23558, .23638,24837, .24941))
/gene="P0456E05.4"
complement(join(23558, .23638,24837, .24941))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="contains EST AU162265(E30874)
unknown protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="BAB92605.1"
/db_xref="GI:20804926"
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                                                                                                                          22377. .22536)
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                                                                                                                                                                                                                                 unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
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                                                                                                                                                                                                     WKLILGYLEGDRALWEQELAKKRSOYAAFKEEFLSNEYSEITEQIDROVKRTHEDMHF
FCGDSSFAKSNQESLKNILIIFAKLNAGIRYQGMBELLAPLFFYFRNDPDDKNANFA
BADSFFCHRELSGFRUNFCOKLDNASHGIQGTLSKLSQLVAKYDGELQRYLEITTEI
NPORYAFRWITLLLIOGENWADTIHIWDTLLSDPDGPQGRSIYRDGTGESMYNIETS
VAHAYQSSRNSAVPVVEKLHRCRKAJGAARLQFAAAPFLSPFRSPETTENAEAFFPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YWLASCSDQNQCVAHARWRAYWASIIIIN"

YWLASCSDQNQCVAHARWRAYWASIIIIN"

complement(join(11701. 119960,11998. ,12076,12765. ,12881, 13131. 13310,13459. ,13587,13660. ,13758,14527. ,14631, 15002. ,15131,13421. ,15487,17632. ,17717,17924. ,17952))
/gene="P0456E05:2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'translation="MCCLMPISTCACVCVERQQTQNADWLATPPAPAFAAAFAYYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(11701. .11960,11998. .12076,12765. .12881, 13131. .13310,13459. .13587,13660. .13758,14527. .14631, 15002. .15131,15421. .15487,17632. .17717,17924. .17922))
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GGRFNETVKWALLKHENFDGSLWVGELAQLSKKVIDLDELRMLAAQGVPDGAAVRPTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="contains ESTs AU101913(S0657), AU101912(S0657)
                                                                                                                                                                                          Submitted (14-MAR-2001) Takuji Sasaki, National Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Oryza sativa (japonica cultivar-group)"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
                    Matsumoto,T. and Yamamoto,K.
a nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similar to rabGAP domains protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="P0456E05"

join(9483. 9641,10723. 10785)

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join(9483. 9641,10723. 10785)

/gene="P0456E05.1"

/note="hypothetical protein"
                                                                                            Published Only in Database (2001)
2 (bases 1 to 173699)
Sasaki,T., Matsumoto,T. and Yamamoto,K.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unknown protein"
                              Sasaki,T., Matsu
Oryza sativa nif
clone:P0456E05
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.38015,

gene

CDS

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FEATURES

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Loudished Only in Database (2001)

Sasaki, Va. val.

Sasaki, T., Matsumoto, T. and Yamamoto, K.

Direct Submission

Lise, School of Scholar

Marchiological Sciences, Rice Genome Research Program; Kannondal

Submitted (21.WAR-2001) Takuji Sasaki, National Institute of
Agrobiological Sciences, Rice Genome Research Program; Kannondal

2-1-2, Tsukuba, Ibaraki 305-6602, Japan

(E-mali:tsasaki@idas.affrc.go.jp, URL.http://rgp.dna.affrc.go.jp/,
On Oct 17, 2001 this sequence version replaced gi:13430001.

Genes were predicted from the integrated results of the following:
(October 1998 version). The genomic sequence was searched against

NCBI NonRedundant Protein database, nr

(ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA sequence database at

RGP. Protein homologies of the coding regions were searched against

NCBI NonRedundant Protein database with BLASTP2.0. ESTS represent
                          Institute of Agricultural Science and Technology(NIAST), RDA, 249 Seodun-dong, Suwon 441-707, Korea (E-mail:jhhahn@rda.go.kr, Tel:82-31-290-0308)
Tel:82-31-290-0309, Fax:82-31-290-0308)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AP003436 185095 bp DNA linear PLN 17-APR-2002 Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, PAC clone:P0470A12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA, clone:P0470A12.
                                                                                                                            * NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* 53114 53213: contig of 5313 bp in length 53213: contig of 119191 bp in length 172404: contig of 119191 bp in length 172405 172505 gap of unknown length 172505 174218: contig of 1714 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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/organism="oryza sativa (japonica cultivar-group)"
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Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0470A12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Trach
Spermatophyta, Magnollophyta, Liliopsida, Poales, Poaceae,
Enrhartoideae, Oryzeae, Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="P0456E05"
49037 a 38377 c 37185 g 49417 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Pred. No. 2.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.7%; Score 44;
00.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /variety="Nipponbare"
/db_xref="taxon:39947"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AP003436
AP003436.2 GI:16197551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0
Matches 44; Conservative
                                                                                                                   NIAR.
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ORIGIN
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AP003436/c
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TITLE
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AUTHORS
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JOURNAL
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                                                                                           COMMENT
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                                                                                                                                                                                                                                          /translation="MAASRRLARKLPSLISKHORLISPEIDVEQAAESPASSSSIPLD
PSLPILPLAVSHLSPPSPLPALPSVHASTPALLKTIKRARHHPRLAALDCHILLAAA
SDSPARPDHRITSLLASRLABSRRLPSTPAALLETIKRRARHHPRLAALDCHILLAAA
SDSPARPDHRITSLLASRLABSRRLPSLRADSPLPAEFVNIILRALARLRRHEDTVRFVGE
RAILAFAASGDIPAASDALASLRRAADSPLPAEFVNIILRALARRRHEDTVRFVGE
MTSTRKVHPDVTYFRNILINSCRABGVDAANRFGERRRSCSPTGVSFTILMRGFFR
FDCLDLVSELCKYRNVEKAVETVELILERWNVSCGCVPAGVTVLECLMKEGKLDKACO
MMGRAVAAETVPDTISCNYIFEALCEAGRYVDANLRLQARKRGFOADGFFYSIIVOG
GOMPLEMENT(10.55150,55176..55310,55441..55668))
COMPLEMENT(10.16(4710..55150,55176..55310,55441..55668))
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iminar to Arabidopsis thallana chromosome 5, At5914420
                                                                                                                                                                                                                          /translation="MGGGGSRSPRDGSGHGRYGHSPSFQQQWGGGGGGGGGGGGGTYPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC091071 174218 bp DNA linear HTG 27-MAR-2001 Oryza Sativa (japonica cultivar-group) chromosome l clone P0456E05, *** SEQUENCING IN PROGRESS ***, 3 ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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Oryza sativa (japonica cultivar-group).
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridplantue; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryzaa.
I (bases 1 to 174218)
Lee, J.-S., Hahn, J.-H., Yoon, U.-H., Lee, M.-C., Yun, D.-W., Kim, H.-I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (Dases I to 174218)
Hahn, J.-H., Eun, M.Y. and Kim, H.-I.
Direct Submission
Submitted (27-MAR-2001) Rice Genome Sequencing Project, National
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 44; DB 8; Length 1/3/
Pred. No. 2.5e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa PAC P0456E05 genomic sequence
                                                                                                                                                                                   /protein_id="BAB92608.1"
/db_xref="GI:20804929"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="BAB92609.1"
/db_xref="G1:20804930"
                                                                                                                                           unknown protein"
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100.0%; Pre
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Best Local Similarity 100.0
Matches 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HTG; HTGS_PHASE2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
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AC091071
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41290. 41359,41646. 41710,42307. 42361,42603. 41176,42818. 42906,43104. 43173,43622,40913. 41002,41120. 41176,43818. 42906,43104. 43173,43622. 43723,43820. 43909,43909,44580. 46604,46714. 46836,44713. 44799,46231. 46311,46819. 46799,46231. 46311,4690470A12.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 join 40309. .40472,40627. .40822,40913. .41002,41120. .41176,
41290. .41359,41646. .41710,42307. .42361,42603. .42730,
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46380. .46604,46714. .46836,46920. .47036)
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/translation="MAAAGGIPASATLLLLVIAAVAVAPLASAVRPVSDAHRSAAAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LUTGKVKALTERVKKNOLPTAGGIGYLEAKHHLLASKODINYYLLKRAGLSVEGUD
VYRSLVBIRLFLEKIRPIDKKMEYQIQKLTINAADSGAAGEKEVDYGSEEVRYTPTGG
FLGRGGYQOQHVYKETFQEIDKSGSGRHHHNHNHGNDYLMVRETKVEEDFNTCTGEFR
ERRQSFLLKSD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(join(34470. .34734,34836. .34921,35025. .35117,
35201. .35364,35440. .35601,35682. .35861,35978. .36414,
36513. .36568)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36513. .36568))
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complement(join(34470. .34734,34836. .34921,35025. .35117,35201. .35364,35440. .35601,35682. .35861,35978. .36414,36513. .36568))
RHAARHAVRNEALGYVVVLRHYPSPVAATWTRRKOOCATGAALPRYEAHTIENTTIGE
GEEEHUVRQPPQGGLRTLRLHQQPRRYESTSCARIGGGSRAGEKHPTLNCQHQRHDRT
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complement(23929, .24237)
                                                                                                                                                                                                                                    /protein_id="bab90279.1"
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/translation="MAQYYSEVDHCAEEMNRPPHAGGEHYAVRRESYEEVDEMARAGR
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30998. .31165)}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="p0470a12.6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F7J7_90
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D15893(C1477),C72138(E1066),AU101125(E1066)
similar to Arabidopsis thaliana chromosome'
                                                                                                                                      complement(23929, .24237)
/gene="P0470A12.4"
/note="hypothetical protein"
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                                                                                                                                                                                                                         /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
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                                                                                                                                                         CDS
                     the identified cDNA sequences using BLASTN 2.0 with the corresponding DDBJ accession no. and RGP clone ID.

A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-' and 'like protein. A gene without significant homology to any protein but with EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted with a gene prediction program is classified as a 'hypothetical' protein.

The orientation of the sequence is from SP6 to T7 of the PAC clone. Detailed information on overlap and assembly quality together with annotation of this entry is available at http://rgp.dna.affrc.go.jp/GenomeSeq.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(19564. .19724,21382. .21688,22059. .22217, 22365. .22505,22923. .23035,23239. .23318))
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/gene="p0470A12.3"
/note="hypothetical protein"
/codon_start=1
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Spacpprsgrreaggeggsgggggrapvinvttrrsrkpwrdssggrrdhaasrhdsiht
rertnwngaiklrpffygtrefrckpslvytpiwagilgchlcvlarllclroormr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /trapesaiation="mexclaiderssglprsnegmrllfsavigvmlgylfgispptvn
vtrlhepssiisylendsgittqtilnhawtsanskrrnnsesnsdeipriyvenny
vtrlhepssiisylendsgittqtilnhawtsanskrrnnsesnsdeipriyvenny
kgaeglapgivvpetdlylrringersedlysoprijetyrgysokrandbavkrffs
bentimletylogrynnwobefewskraihvsvrrqtkwytakrelhpdivapydyiffw
bedlsvqhfraralttvrkingleisopglepprgitwwytklgdoguykvyterpw
wctdphlepcaafveimatvfsrdawkcvwhmiqudlyhgwgidfalkrcyepahekt
gvvdsqwvihqvipslignogtaengrtpwegvrarckewgmegvrrladaeskayyigk
                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Oryza sativa (japonica cultivar-group)"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  similar to Oryza sativa chromosome 5, P0574H01.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(15118, .16344)
/gene="P0470A12.2"
complement(15118, .16344)
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unknown protein"
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/db_xref="GI:20161352"
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/clone="P0470A12"
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HTG; HTGS_PHASE1.
                                                                        /chromosome="1
                                                                                                                                                 Query Match
Best Local Similarity 100.0
Matches 44; Conservative
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Rattus norvegicus
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KNDIVKLFDT KSYDDGTFYFDERHVDAAEYKGPITTSASVVRGYTSFAAARAGKLAIV
RCHIGLARFFLGIGLEGSAADCFNOIEVEPPLVLSLPSKVFSLTSKDQLKVEVTTV
FGSAAPPLRVNLVVQLSSDSKVITTTTRELCPDLDNNVHYLDIAPLKLSVDGKVEVTTV
ISLOEOEHFTIYATGGTNTEALFYTGLIKVDKAEIGISDNNAGTVESVQK NDLQKDYS
DSLANHLQKLRLSFOLSTPLGKTFRPHQVFLKLKHDESKVEHLFVVPGSSQKDDLQKDTS
DFLGIVERFYYLSGRYDLEAVGDAAMENSFLASCHHIEDDLEAPEKRAPKRPRQAND
PFSKFGPKREISHIFRSPEKRPPRELSFAFTGLTLLPIUFBAPRKRAPKPPGAND
PRAARARSLFHAGIGAVLLYVLFWIKLDLFTLKYLSFLGYFLUFGLNLKPPSL
SAKQKTA"
                                                                                                                                                                                                                                                                   complement(join(47978. .48051,48179. .48239,48314. .48378,48478. .48759,48377. .48911,49020. .49094,49242. .49298,49552. .49655,49763. .49964,50111. .50213,50317. .50378,50507. .50561,50738. .50841,50926. .51048,51175. .51219,
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clone P0470A12,
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Oryza sativa (japonica cultivar-group).
Eukarya viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoldeae; Oryzeae; Oryza.
I (basea; 1 to 185481)
Lee,J.-S., Hahn,J.-H., Yoon,U.-H., Lee,M.-C., Yun,D.-W., Kim,H.-I.
                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                         7:7%; Score 44; DB 8; Length 185095;
                                                                                                                                                                                                                                                                                                                                                                                                                                       AC091088 185481 bp DNA linear Oryza sativa (japonica cultivar-group) chromosome 1 *** SEQUENCING IN PROGRESS ***, 4 ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                     2.5e-12;
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Best Local Similarity 100.0%; Pred. No. 2.56
Matches 44; Conservative 0; Mismatches
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AC091088.1 GI:13487944
HTG; HTGS_PHASE2.
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Ratus, ö A linear HTG 23-JUL-2002 \*\*\* SEQUENCING IN PROGRESS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Gaps 1. .185481 /organism="Oryza sativa (japonica cultivar-group)" ö Length 185481; 374 others 7.7%; Score 44; DB 2; L6 100.0%; Pred. No. 2.5e-12; ative 0; Mismatches 0; Rattus norvegicus clone CH230-274116, \*\*\*, 77 unordered pleces. 41493 g 50653 t /variety="Nipponbare" /db\_xref="taxon:39947"

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COMMENT

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31263
32587
                                                                                                                                                                                                                                                                                    NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 77 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                               Submitted (01-MAY-2002) Human Genome Sequencing Center, Department Submitted (01-MAY-2002) Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 185133) Morley, K.C. Direct Submission Genetics, Baylor College of Medicine, Department Submitted (23-UL-2002) Human Genome Sequencing Center, Department Submitted (23-UL-2002) Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 18, 2002 this sequence version replaced gi:20467917.
                                                                                                                                                                                        Center project name: GWLC
Center clone name: CH230-274116
Center clone name: CH230-274116
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap, version 0.990329
Consensus quality: 120616 bases at least 030
Consensus quality: 127908 bases at least 030
Consensus quality: 132518 bases at least 020
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Contact: hgsc-help@bcm.tmc.edu
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1101: gap of unknown
2138: contig of 1037
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22169:
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                   Worley, K.C.
Direct Submission
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/translation="MSGRGKQGGRARAKAKTRSSRAGLQFPVGRVHRLLRKGNYAERV
GAGAPYYLAAVLEYLFAEILELAGNAARDNKKTRIIPRHLQLAIRNDEELNKLLGKVT
1804GYULPNIQAVLLPKKTSHKKKKK"
33 39 208 t
                                    Web site: http://www.isc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Akhter,N. ayele.K. Beckstrom-Sternberg,S.W., Benjamin,B.,
Blakesley,R.W., Bouffartom-Strom-Sternberg,S.W., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighl,P.,
Marsen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,O.L., Maskelloc., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                           Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAR Plate: 69 Row: p Column: 22
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 15718718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AY102542 1275 bp mRNA 11near PLN 13-AUG-2002 Arabidopsis thallana hypothetical protein (At2g23370/F2686.2) mRNA, complete cds.
AY102542
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Varidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1275)
3 Aso,Y.., Ishmael,N., Kumar,N., Redman,J., Riedmuller,S.,
Utterback,T., Whittelaw,C.A., Fraser,C.M. and Town,C.D.
Cloning and sequencing of full-length cDNAs for hypothetical genes
from chromosome 2 of Arabidopsis thaliana
Dipublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xiao,Y., Ishmael,N., Kumar,N., Redman,J., Riedmuller,S.,
Utterback,T., Whitelaw,C.A., Fraser,C.M. and Town,C.D.
Direct Submission
Submitted (08-MAY-2002) Plant Genomics, The Institute for Genomic
Research, 9712 Medical Center Drive, Rockville, MD 20850, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1138;
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/note="Yector: pCMV-SPORT6"
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                      Gaithersburg, Maryland;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Strausberg, R.
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Submitted (06-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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                                                    Length 185133;
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91514: contig of 1671 bp in length
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Contact: MGC help desk
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
                                        'Match 5.4%; Score 31; DB 2; I
Local Similarity 100.0%; Pred. No. 2.2e-05;
les .31; Conservative 0; Mismatches 0;
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Sequence 508 from Patent W00210453.
AX400832
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2 (bases 1 to 1450)
Tanguay, R.L. and Vasiliou, V.
Direct Submission
Submitted (15-AUG-2000) School of Pharmacy, University of Colorado
Health Sciences Center, 4200 East Ninth Ave, Box C238, Denver, CO
                                                                                                                                                                                                             KAOPPKHLMOLLNIFTARGKSIVSPCAKOGLIJPLTIPLVKMSPGSSTALLERPPAPSS
MEMPVVEVQKHGVWFLANNVDOFIHRILVEEDVSKPERCSOBIFNAAGEAGKKLYSKG
PRESSSRLMDLDAYLLEKVGLEPPSLEREKVIRHIJENGDHVSALVATEFYTKRGNFPGFA
RPFAFNAKVLLKLGRHLEARDARGALKSSWWTLGCRYEEIAQIAEWGEEQIAOYKER
VTGEGKQRDIDRGKFWAQASLIDEAAFLLNLASLEGTWDESLERVAQCYKEAGLNDIAK
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                                                                                                                                                                                                /translation="MHRGAAVFGRKRRLILLHGSRNFARSFCSSSSLSEHECFIKDIA
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Identification and characterization of the zebrafish alcohol
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   /organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
/chromosome="2"
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                                                                                                                                          /evidence=not_experimental
/product= hypothetical protein"
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/db_xref="G1:21805665"
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232 c 308 g 348
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                                                                            /gene="At2g23370/F26B6.2"
29. .1051
                                                                                                             /gene="At2g23370/F26B6.2"
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                                                  /note="ecotype: Columbia"
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/organism="Danio reri
/db_xref="taxon:7955"
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clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 18 Row: j Column: 2 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6755673. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus, staufen (RNA-binding protein) homolog 1 (Drosophila), clone MGC:13708 IMAGE:4188394, mRNA, complete cds. BC012959 BC012959.1 GI:15277959
/product="alcohol dehydrogenase"
/protein_id="aAK97853.1"
/db_xref="d1:1542878"
/db_xref="d1:1542878"
/translation="maragkyrecranvawepraplumbelevappoggelrikviat
/translation="maragkyrecranvecoppyrdsyrpspkropsyrpkredgkyr
GLCHTDLYHLVDGDKRGFPVVLGHESAGVVESVGPGVTLOFRFGREDKYPELSOGGKK
GLCHTDLYHLVGGSSWAFKFUDIMAEPTSFRFTCRGQTILQFWGTSFFSFTVINONAVA
FCCRCPKTNLCESSWAFKFUDIMAEPTSFFTCRGQTILQFWGTSFFSTFTVINONAVA
FLANDINEKKFEKARVFGATDFLNPKAFNKPISEVLIEWTNGGGYDFSIECTGNTEV
MRSALESCARGWGVSVVVGWTRNDENNEAPROLITGKTWKGSLFGGFRCKDSVFKLVR
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MRSALESTARGWGTSFFTTHMALEQVNDAINLANGTGGIRTIMTVSK"

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musimusia; La 2879)
Strausberg, R.
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/lab_host="DH10B"
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Submitted (20-MGG-2001) National Institutes of Health, Mammalian
Submitted (20-MGG-2001) Cancer Genomics Office, National Cancer
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Email: capabs.remail.nth.gov
Email: capabs.remail.nth.gov
Inssue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
contact: amadan@systemsbiology.org
Anny Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anurack
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
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Pred. No. 0.00023;
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100.0%; Pred. No. c.
. 0; Mismatches
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/organism="Mus musculus"
/db_xref="taxon:10090"
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Gaps

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Length 3194;

Dear, P., Kumpf, K.,

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Dictyostellum discoideum chromosome 2 map 109820-140341 strain AX4, AC115592
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VYLNDEEIEVLETKGSSIQQLELLDTTKFGSIDVISGDSNGMLVIFSNHQILYEDTLN
GSITSIITHRLSIGDSLGLVTSIKPHQNALWRYKIPSVNQTLNSLIDSDIJAINPNIK
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RYIGEFEIVDDHRSGKIVIDLIGRINKCGVISPRFDVTLDEIEKWASYLLPSRQFGHI
VLTTSLGIMDHNEARTRHTGGKLLGFFY"
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/note="ORF_ID:dd_01555"
/codon_start=1
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Dictyostellum discoldeum.

Dictyostellum discoldeum

Eukaryota: Mycetoza; Dictyostellida; Dictyostellum.

1 (bases 1 to 30523)

1 (bases 1 to 30523)

Lebmann, R., Baumgar, C., Parra, G., April, J.F., Gulgo, R., Kumg-Tunggal, B., Cox, E., Quall, M.A., Platzer, M., Rosenthal, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Agency : Deutsche Forschungsgemeinschaft (DFG).

* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (http://genome.imb-jena.de/dlctyostellum/)
and the Univerity Colonge, Institute for Blochemistry I
(http://www.uni-koeln.de/dictyostellum/project.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence and Analysis of Chromosome 2 of Dictyostellum
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/protein_id="AAL92278.1"
/db_xref="G1:19569976"

    30523
    /organism="Dictyostelium discoideum"

               DB 9; LO
5.1%; >cc. 100.0%; Pred. No. c. 0; Mismatches
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/note-"ORF_ID:dd_01553"
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                                                         29; Conservative
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       Query Match
Best Local Similarity
Matches 29; Conserva
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AC115592/c
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                                                                                                             LRRLPPLPAVERVRPRIKKKSOPTCKLOTAPDYGGGNNPISKLAGIOQAKKEKEPEYM
LLTEKGLPRRREFVMQVKVGHHTAEGYGTNKKVAKRNAAENMLEILGFKVPGAOPAKP
ALKSEKRTPVKKRGDGRKYTPFEPSRGDENGTSNKDEFRMPYLSHQQLPAGILPMVP
EVAQAVGVSGHHTKDFTRAAPNPAKATVTAANTARELLYGGTSPTAETILKSNISSGH
VPHGPRTRPSEQLYLYLERAGGFOVEKYDFPKNNKNEVYSLINGSSQPPLVSHGIGKDV
ESCHDWAALNILKLLSELDQGSTEMPFTGNGFVSACGRC**

735 C 699 g 647 t
                                         /trānslation="MYKPVDPHSRMQSTYSYGMRGGAYPPRYFYPFPVPPLLYQVELS
VGGODFNGRGKMRPPVKHDAPARALRTLQSEPLPERLEVNGREAEEBNINKSEISQVF
EIALKRNLPVNFEVARESGPPHMKNFVTRVSYGEFVGEGEGKSKKISKKNAARAVLEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (19-AUG-2000) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:chaidimal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
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3194 bp mRNA linear PRI 29-SEP-2000
HOMO Saplens CDNA: FLJ21866 fis, clone HEP02379, highly similar to
AF061938 Homo saplens staufen protein (STAU) mRNA.
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Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T.,
Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
NEDO human cDNA sequencing project
Unpublished
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sugano, S., Suzuki, Y., Ota, T., Obayashi, M., Nishi, T., Isogai, T., Shibahara, T., Tanaka, T. and Nakamura, Y.
Direct Submission
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/note="highly similar to AF061938 Homo sapiens staufen
protein (STAU) mRNA"
a 787 c 732 g 781 t
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5.1%; Score 29; DB 10;
Best Local Similarity 100.0%; Pred. No. 0.00023;
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/note="cloning vector pME18SFL3"
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/cell_type="hepatoma"
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complement(join(11012. .11317,11409. .11524,11604. .11766))
/note="ORF_ID:dd_01558"
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INNDAHNQTLTQHTDLEHVDLESDSKNIKYQQQQQQHOHQQHQQYQQQHQQQHQQCNNN
NNNNGYINPHLTESSQLFSSVPLNSLPNSPYHINYPYTNNNSNSNNSYNNTNSNNNNN
GNDVYSENNNSNNNNKKKYKKKKKKRKRNIFKKKQDKESDLMKSNIPIIIKDNDDD
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Elvkofnykkrplaavchgaqvlaanivsgikctaypacrebgvqaggiyqblavbd
VydbhlykoskawpchkkligleikLlgtifhu"
complement(joln(1238). 16761,16921. 18037))
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ETIDWLSDIETGGCSILNIRDTLHSKLKOMKLDFSTSELLEYARIKFKQVIPILDSNK
KLPSIHILRTHDDIVSLINKLNESNFIDNENLFKYYMIQLIOFGSRNSNKYQRSICDN
VGEIDLVLETMVEHFNIEEVSQGAYIQVHDDFNKYKLFTÖQIINLSKLKVNVNHFPNA
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QYLIDKFLEGPLSFTNLLLILNFLYLKLIRVNNLTIDQIKTAYQLISNYIEINRSKLT
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IDIIIQNNKPYQTIKQLFQLLVNETKSIVLYARYLKEYNELIETIETCRQIQLLLMYF
MTKTYNTNVLMFLLKKDLHIKLTSNYCEPYLDILFGCNQIDKTNIIIFYNTYKSQKSI
SPVNCMCIGYFDSNLSTSSPSSNASSNSNGTSSSSASLSPQIALGCENGFITLLVDFK
IYPYCQIGYPITKLNKMKYSDINNNDNDNNYNGNNNSNGDDDDDDDDDLDILICTGY
FNSIKMFYNKEVICDHSLDDWCHTLSIGQVENNGDKTIVIGKLDNTIEYLKPFKLIKK
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DSMLKHKQYQILICKLKANENLNFKSTYRIIEKIYEIKDIELFKEINSLLLTNGYQED
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INDSKPFTLTEIERSYFIGEYSEIGKHRDQEIIEEMIKMISNIPISSTSILGTREYKV
                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="mnnecneySekLFWRIFKNKYLLNCIFKNKCCHKSKKFKTIASI
NSILKHKQYQLLVCKLKANENLYFNNTYRIIEKIYEIKDIELFKELNSLLLTKGYQED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INDSKPFTLTEIERNYFIGEYSEIGKHRDQEIIEEWIKMISNIPISPTSILGTREYKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IEDVKGELGYISSSIDSVLLYFEFYYCNYHVNSKSKSIPTSIQTQIDII1QNNKPYQS
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                                                                                                                                                               .5169,5377. .6077,6139. .6530,6628. .7348
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                                                                                                                                                                                                                                                                                                             /protein id="AAL92280.1"
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                                                                                                                                                                                                       7577. .7592)
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CDS

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//Lranslation="WINTERCYTLDKYFERDNGMPDRNQFKITTCKFDENQKMEKDQIM
IKLEYVSVDPYLRARMNSKKTFVDPFKLHDPINSGCIGKVLKSTSRFKEGETLVVGAF
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PNGIDIFYENVGGEVTDDIGQRAQIYFEKRITMQFFLVPFYSSGLNYHSPTYABDLKKAC
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IDDLAMNHDNSKSHHNFNGGTNSGCSVIPKYQAASPDEESLTLTAARYGFILKSREDN
IITISVHGREERFELLNVLEFNSTRKRMSVIVKNQKNQIKIYCKGADSVIFERAKKNT
                                                                                                                                                                                                                                                                                                                                                                   DHCVGILLGSTEKHLSEFACSGIRTLCMSVRTIEHEETTAWNKIHQEASISLVKKAEKV
DAACELIEKDLLLIGSTGIEDRLQDHYPETISALREMGIKWYUTGRKOETAISISTS
SAVINEMEHELIILNESNKQALMKRLITISINEKKHHFNDMSGRWGSVKYLEKVA
SKLRLEPSDAPNLLNKSNGMARAVANSQKHTAIILOSTLALALEDLIKYFFLQVAR
TCESVVCCRCSPSQRAVVNLVAERSFLEGDGAITMSIGDGANDVPMIQKAHVGVGIS
GREGMQAVLASDFAIANFSMIRRLIIVHGNRSYRMYKLIIVSFSKNIALSISQFWFG
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ITTOPPFLLYSNINOKPOPOLOGOGOGOGOGOGOGKRKLPPHKSOSSPSINRSSP
IKOLEDLSSDAALFYNYOSSPSQHHHQQIQOQOQYYDLNDYONYFSTNEGNYIIIS
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AKSSISKCQWIKGAKDLDDFSCKVDYEGPNNDIYSFDGVLTILKGFERSNIGDSTVVP
TTNYVPVSIDQLLLRGTKLRNTDWYIGVVTYSGVDTKIEKNASKASQKRSSVERGVNN
KLLILFLLQTIICIICSIGHNRWHLEDDKDAKPWYIDYDPEQTEDFIYVSYVILYNTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FFSGFSGOMIYEDFLETLYNALFTSLPVIFLGTFDQDTKEDDLLNKPYLYRVCQSNSP
FSTWKFIWWYFIGMWOSATIFFVTFFVMNTSTIEGGKTLGLWSIGTAAYIYLVVTVNL
                                                  GLNNNHNNNNEQITSSVATSTDKSQLLSMKTNQVITSKYNVFTFIPKVIFYOFSRLA
NLYTLAIVILCMFSFSPVGPVSSLTPLLVVIAVTSFKELAEDLKRHKODKEINGRETS
                                                                                                                                                                                                                                        IPLSMYVSMEMIRVSNAHFIDSDLEMYDESTDTPAQARNTNINEELGQIQYLFSDKTG
TLTCNEMVFNRCTIGGQVYGPEDSSLQDLRLFIKNQLSDSSNGSYLRQSNGLSGGGG
LKLFVSVVSLQDPSDNSLILLTASLVGSFDIERDESASSSSQAKASRCIFFYGSDVK
                                                                                                       IYRPPFYIISPTASKEDLKRRQSGFNGFISRIGNFFGSIKQQYIQTEKNIPMVPDNDY
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Pred. No. 0.00025;
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/db_xref="GI:19569983"
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ISM Chloroplast Lasthenla gracilis
Chloroplast Lasthenla gracilis
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae; eusaterida II; Asterales; Asteraceae; Asteroideae;
Helenieae; Lasthenla.

I (bassa 1 to 410)
RS Chan, R., Baldwin, B.G. and Ornduff, R.
Cryptic goldfields: A molecular phylogenetic re-investigation of
Lasthenla californica sensu lato and close relatives (Compositae:
Heliantheae sensu lato)
AL Am. J. Bot. 89 (7), 1103-1112 (2002)
CE 2 (bassa 1 to 410)
CE 2 (bassa 1 to 410)
CE 2 (bassa 1 to 410)
CE 3 (ban, R., Baldwin, B.G. and Ornduff, R.
Direct Submission Ornduff, R.
Chan, R. Daldwin, B.G. and Ornduff, R.
California, 1001 Valley Life
Integrative Biology, University of California, 1001 Valley Life
Coating R.
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California, 1001 Valley Life
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           Direct Submission
Submitted (23-APR-2002) DOE Joint Genome Institute, 2800 Mitchell
Submitted (23-APR-2002) DOE Joint Genome Institute, 2800 Mitchell
Drive, Wahlut Creek, CA 94598, USA
On Apr 23, 2002 this sequence version replaced 91:19224972.
Draft Sequence Produced by DOE Joint Genome Institute
Www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www-shgc.stanford.edu
Quality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 0.3.
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Lasthenia gracilis isolate calil53 tRNA-Lys (trnK) gene, intron; and maturase K (matK) gene, partial cds; chloroplast genes for
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    Joint Genome Institute and Stanford Human Genome Center.
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/db_xref="taxon:182806"
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5.1%; Score 29; DB 9; Le
Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 29; Conservative 0; Mismatches 0;
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56281 a 29916 c 30420 g 56206
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AF467161.1 GI:21759599
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/codon_start=2
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DOE Joint Genome Institute.
DIRECT SUBLISHED
Submitted (15-NOV-2001) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 112226)
DOE Joint Genome Institute and Stanford Human Genome Center.
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                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 112226)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (01-JAN-2002) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Greek, CA 94598, USA
On Jan 1, 2002 this sequence version replaced g1:16930902.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 172823)
DOE Joint Genome Institute.
Dorect Submission
Submitted (07-MAR-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 172823)
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Eukaryota; Metasoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 172823)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                       AC099486 112226 bp DNA linear PRI 01-JAN.
Homo sapiens chromosome 5 clone CTD-2011G10, complete sequence
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Homo sapiens chromosome 5 clone RP11-93N19, complete seguence
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Finishing Completed at Stanford Human Genome Center
www-shgc.stanford.edu
Quality: Phrap Quality >-40 99.8% of Sequence;
Estimated Total Number of Errors is 0.2.
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Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 29; Conservative 0; Mismatches 0;
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36508 a 19376 c 19390 g 36952 t
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1. 11226
7. Crganism="Mono sapiens"
/db_xref="taxon:9606"
/chromosome="5"
                                                                                                                                       AC099486.2 GI:18030138
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AC114323.2 GI:20270116
                                                                                                                                                                                                                                                                                                                Direct Submission
Unpublished
                                                                                                                                                                                      Homo sapiens
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                                                                                       DEFINITION
ACCESSION
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ORIGIN
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AC099486
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Search completed: June 16, 2003, 07:56:05 Job time: 1698.8 secs

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June 16, 2003, 06:35:31; Search time 39.9504 Seconds (without alignments) 4406.275 Million cell updates/sec
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-998-416-981
US-08-998-416-981
US-08-950-720A-1
US-09-280-116-85
US-09-280-116-85
US-09-280-116-1
US-08-942-218A-1
US-08-942-218A-1
US-08-116-1
US-08-116-1
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US-09-031-563-1
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US-08-688-417-5
US-08-688-417-5
US-08-688-417-5
US-08-688-417-6
US-08-688-417-6
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US-09-175-928-34
US-09-180-116-166
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US-09-091-097-5
                                                                                                                                                                                                                                                                                                                                            441362 seqs, 153338381 residues
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                                                                       OM nucleic - nucleic search, using sw model
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 2000000000
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Match
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Perfect score:
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Sequence 12, Appl Sequence 5, Appl Sequence 12, Appl Sequence 1, Appl Sequence 7, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 19, Appl Sequence 17, Appl Sequence 17, Appl Sequence 11, Appl Sequence 2, Appl Sequence 25, Appl Sequence 3, Appl Sequenc	g Human Protease Homologs	Length 212; ; Indels 0; Gaps 0;	ASHBYA GOSSYPII
749 4 US-09-257-583-12 810 4 US-09-257-583-12 944 4 US-09-227-357-122 1132 3 US-08-894-731-3 1164 2 US-08-935-674B-7 1154 4 US-09-395-674B-7 1353 4 US-09-286-529-6 1353 4 US-09-244-3-184-44 1454 4 US-09-34-46-3 1619 2 US-08-91-94-8 1619 2 US-08-91-91-94-8 1619 4 US-09-354-465A-1 2191 4 US-09-254-465A-1 2191 4 US-09-299-913-25 2191 1 US-08-233-005-3 2197 1 US-08-233-25	BULT 1:  -09-280-116-50  -09-280-116-50  -actent No. 6331427  -actent No. 630-24, 035800/176965  -actent Application Number 105/09/280,116A  -actent Application Number 105/09/280,116A  -actent Number OF Seq 10 Nos: 268  -actent No. 60  -actent No	5%; Score 26; DB 4; .0%; Pred. No. 0.028; 0; Mismatches 0 CACGCGTCGC 26 	B416  NA SEQUENCES OF FHEREOF  Corporation  1
22222222222222222222222222222222222222	SULT 1  1-09-280-116-50 Sequence 50, Application US/09280116A Patent No. 6331427 APPLICANT: Robison, Keith E. TITLE OF INVENTION: NUCLEIC Acid Mol. FILE REFERENCE: 5800-74, 035800/1769 CURRENT APPLICATION NUMBER: US/09/28 CURRENT APPLICATION NUMBER: US/09/28 CURRENT APPLICATION NUMBER: US/09/28 CURRENT PAPLICATION NUMBER: US/09/28 CURRENT PAPLICATION NUMBER: US/09/28 SOFTWARE: PATENTIN Ver. 2.0 SEQ ID NO 50 LENGTH: 212 TYPE: DNA ORGANISM: HOMO SAPIENS FEATURE: CTHER INFORMATION: Zinc carboxypepti	Match ocal Similarity 100 s 26; Conservative 1 ACCCACGCGTCCGCC	11, 622, 622, 11, 11, 11, 11, 11, 11, 11, 11, 11,
	RESULT 1. US-09-280-1 ; Sequence ; Patent NO ; GENERAL I ; APPLICAN ; TITLE OF ; FILE REF ; CURRENT ; CORRENT ; CORRENT ; CORRENT ; CORRENT ; TYPE: D) ; ORGANIS; ; FEATURE ; COTHER II	Query Match Best Local S Matches 26 Oy 1	RESULT 2 US-08-998-416 Sequence 98 Sequence 98 Septence No. GENERAL IN APPLICAN APPL

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Score 26; DB 4; Length 717;
Pred. No. 0.023;
                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
ATTORNEY AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 82/21
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMUNICATION INFORMATION:
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 904:
SEQUENCE CHARACTERISTICS:
LENGTH: 717 base pairs
TYPE: nucleic acid
STRANDENNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/950,720A
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                                                                                                                                                                                                                                                                                                                                                                                                                                            549 ATACTAAAAAAAAAAAAAAAAAAAA 574
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APPLICANT: Lofton-Day, Catherine E.
APPLICANT: Lok, SI
APPLICANT: Jaspers, Stephen R.
TITLE OF INVENTION: INSULIN HOMOLOG
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Bastlake Avenue East
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08950720A Patent No. 6046028
                                                                                                                                                                                                                                                                                                                                                   4.5%; Scur.
100.0%; Pre
                                                                                                                                                                                                                         , MOLECULE TYPE: DNA (genomic)
, ORIGINAL SOURCE:
, ORGANISM: PAG1563UP
, US-08-998-416-904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: SAWISIAK, Deborah A
REGISTRATION NUMBER: 37,438
REFERENCE-POCKET NUMBER: 97
TELECOMMUNICATION INFORMATION
TELEPHONE: 206-442-6672
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COMPUTER: IBM Compatible
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SEQUENCE CHARACTERISTICS:
LENGTH: 792 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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Best Local Similarity 100.
Matches 26; Conservative
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STATE: WA
COUNTRY: USA
ZIP: 98102
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APPLICANT: Wendland, Jurgen
APPLICANT: Knechtle, Philipp
APPLICANT: Rebischung, Corinne
APPLICANT: REBISCHUNG, CORINNE
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 638;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                  NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOORER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFRAX: 919-541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.5%; Score 26; DB 4;
100.0%; Pred. No. 0.024;
tive 0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: No. 6239264artis Corporation STREET: 3054 Cornwallis Road CITY: Research Triangle Park STATE: No. 6239264th Carolina COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              549 ATACTAAAAAAAAAAAAAAAAAAA 574
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CURRENT APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CTASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: CH 0016/97
                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                    981:
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Pohlmann, Rainer
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SEQUENCE CHARACTERISTICS:
LENGTH: 638 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 26; Conservative
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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ORIGINAL SOURCE:
ORGANISM: PAGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-998-416-904/c
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APPLICANT:
APPLICANT:
APPLICANT:
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NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,031
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; LOCATION: (95)...(959)
US-09-372-422A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Zea mays
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APPLICANT: Robison, Keith E.
APPLICANT: Robison, National Applicants Robison, Mail Applicants Robison, National Applicants Robison, National Applicants S800-24, 035800/176965
CURRENT APPLICATION NUMBER: US/09/280,116A
NUMBER OF SEQ ID NOS: 268
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 85
LENGTH: 1021
                                                                                                                                                                                                Gaps
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Fatent No. 6323334
GENERAL INCHARITOR
APPLICANT: KINGSDUTY, G.
APPLICANT: Leiby, K.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: TREATMENT OF IMMUNE DISORDERS
FILE REFERENCE: 7853158
CURRENT APPLICATION NUMBER: 0S/09/560,639
CURRENT APPLICATION NUMBER: 60/155,862
EARLIER APPLICATION NUMBER: 60/155,862
SERLIER APPLICATION NUMBER: 60/155,862
SEALLIER PILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                      Query Match
4.5%; Score 26; DB 3; Length 792;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 26; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                       42 ACCACGCGTCCGCCACGCGTCGC 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: misc_feature
; LOCATION: (1)..(1021)
; OTHER INFORMATION: n = a, t, c or g
US-09-280-116-85
; FEATURE: Coding Sequence
; NAME/KEY: Coding Sequence
; LOCATION: 77...481
; OTHER INFORMATION:
US-08-950-720A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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; LOCATION: (84)...(557)
US-09-560-639-12
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US-09-280-116-85/c
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LENGTH: 1210
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    Length 1210;
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Ouery Match 4.5%; Score 26; DB 4; Length 121
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 26; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                               Sequence 17, Application US/09372422A
Fatent No. 6313375
GENERAL INFORMATION:
APPLICANT: HORDAYION:
APPLICANT: Francois Barrieu
APPLICANT: Francois Barrieu
TITLE OF INVENTION: Malze Aquaporins and Uses Thereof
FILE REFERENCE: 0919-08-11
CURRENT APPLICATION NUMBER: US/09/372,422A
CURRENT APPLICATION NUMBER: US 60/098,692
PRIOR APPLICATION NUMBER: US 60/098,692
PRIOR APPLICATION NUMBER: US 60/098,692
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 1384
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ZIP: 19482
ZIP: 19482
COMPUTER READABLE FORM:
MEDUM TYPE: Diskette
COMPUTER: IBM Compatible
GORBATING SYSTEM: DOS
SOFTWARE: FastEG for Windows Version 2.0
CURREMT APPLICATION DATA:
APPLICATION NUMBER: US/08/942,218A
TILNG DATE: 01-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4;
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Patent No. 5935835
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: McCarte-Roshak, Amy
APPLICANT: Marshall, Lisa
TITLE OF INVENTION: Human Myt-1 Kinase Clone
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & Prestia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 4.5%; Score 26; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 26; Conservative 0; Mismatches
                                                                                    1 ACCCACGCGTCCGCCCACGCGTCCGC 26
                                                                                                                  5 ACCCACGCGTCCGCCCACGCGTCCGC 30
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STREET: P.O. Box 980
CITY: Valley Forge
STATE: PALEY FORGE
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030,389
FILING DATE: 11-OCT-1996
ATTORNEY/AGENT INFORMATION:
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US-08-724-394A-15/c
; Sequence 15, Application US/08724394A
; Patent No. 5872237
PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                            TELEPHONE: (908) 654-5000
TELEFAX: (908) 654-7866
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 2205 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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; LOCATION: (300)...(2414)
US-09-409-180A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear FEATURE:
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LENGTH: 2864
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Sequence 1, Application US/09280116A

Patent No. 6313427

GENERAL INFORMATION:

APPLICANT: Robison, Keith E.

TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
FILE REFERENCE: 5800-24, 035800/176965

CURRENT APPLICATION NUMBER: US/09/280,116A

CURRENT FILING DATE: 1999-03-26

NUMBER OF SEQ ID NOS: 268

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1

LENGTH: 1504
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| Sequence 41, Application US/08888077A
| Patent No. 6020143
| Patent No. 6020143
| Patent No. 6020143
| Patent No. 6020143
| APPLICANT: ST. GEORGE-HYSLOP, PETER H
| APPLICANT: ST. MENSER, PAUL E
| TILLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
| TILLE OF INVENTION: TO ALZHEIMER'S DISEASE AND USES THEREFOR.
| NUMBER OF SEQUENCES: 41
| CORRESPONDENCE ADDRESS: 41
| CORRESPONDENCE ADDRESS: 51
| ADDRESSES: LERNER, DAVID, LITTENBERG, KRUMHOLZ & MENTLIK
| STREET: 600 SOUTH AVENUE WEST
| CITY: WESTFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1504;
                                                                                                                                                                                                                                                                                                                        Score 26; DB 2; Length 1448;
Pred. No. 0.021;
0; Mismatches 0; Indels
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4.5%; Score 26; DB 4;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 26; Conservative 0; Mismatches (
                                                                                                                                                                                                                                                                                                                             Query Match 4.5%; Score 26; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 26; Conservative 0; Mismatches
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    REFERENCE/DOCKET NUMBER: ATGTELECOMMUNICATION INFORMATION:
TELEPAX: 610-407-0700
TELEFAX: 846.69
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
LENGTH: 1448 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                       MOLECULE TYPE: CDNA
US-08-942-218A-1
                                                                                                                                                                                                                                         linear
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Gaps
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SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/888,077A
FILING DATE: 03-4UL-1997
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/592,541
FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: PALISI, THOMAS M 65
REGISTRATION NUMBER: 36,629
REFERENCE/DOCKET NUMBER: SCHERING 3.0-017 CIP CIP IV
TELECOMONINICATION INFORMATION:
ACCOMMINICATION INFORMATION:
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APPLICANT: White, David
APPLICANT: White, David
APPLICANT: White, David
APPLICANT: Slos-Santiago, Inmaculada
APPLICANT: 21106-Santiago, Inmaculada
APPLICANT: 22106-Santiago, Inmaculada
FILE REFERENCE: 5800-59
CURRENT APPLICATION NUMBER: US/09/409,180A
CURRENT APPLICATION NUMBER: US/09/409,180A
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 2864;
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0.02;
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0.02;
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4.5%; Score 26; DB
Best Local Similarity 100.0%; Pred. No. 0.0
Matches 26; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 4.5%; Score 26; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 26; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: 1..2205
OTHER INFORMATION: /note= "mutTM1-TM2"
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Gaps
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                                                                                 OPERATING SYSTEM: PC-UDS/MS-LUS
OPERATING SYSTEM: PC-UDS/MS-LUS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/044,618
FILING DATE: 19930406
CLASSIFICATION: 435
PROR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/07/257,696
ATTORNEY/AGENT INFORMATION:
NAMM: FOX, SAMUBE. L
REGISTRATION NUMBER: 0654.0490001
TELEPHONE: (202)466-0800
TELEPHONE: (202)466-0800
TELEPHONE: (202)466-0800
TELEPHONE: (202)466-0800
TELEPHONE: (202)466-0800
TELEPHONE: ABSE DID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3747 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
4.5%; Score 26; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 26; Conservative 0; Mismatches 0;
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. 0.018;
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APPLICANT: Frederic de Sauvage
APLICANT: Arnon Roshenthal
TITLE OF INVENTION: Fused
FILE REFERENCE: P1272
CURRENT PFLICATION NUMBER: US/09/031,563A
CURRENT FILING DATE: 1998-02-26
NUMBER OF SEQ ID NOS: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3688 ATACTAAAAAAAAAAAAAAAAAAAA 3713
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                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09031563A Patent No. 6022708
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: unknown N
LOCATION: 4160, 4243, 4361
; OTHER INFORMATION: unknown
US-09-031-563-1
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ORGANISM: Homo sapiens
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LENGTH: 4880
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US-09-031-563-1
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Patent No. 5449605
GENERAL INFORMATION:
APPLICANT: SMULSON, MARK
TITLE OF INVENTION: CANCER BY THE USED OF RESTRICTION TO
TITLE OF INVENTION: POLYMORPHISM OF THE GENE FOR THE HUMAN POLY (ADP-RIBOSE):
TITLE OF INVENTION: POLYMERASE
TITLE OF INVENTION: POLYMERASE
TITLE OF INVENTION: POLYMERASE
TITLE OF STREET OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
APPLICAMT: Feder, John N.
APPLICAMT: Kronmal Gregory S.
APPLICAMT: Lauer, Peter M.
APPLICAMT: Lauer, Peter M.
APPLICAMT: Lauer, Peter M.
APPLICAMT: Thomas, Winston
APPLICAMT: Wolff, Roger K.
TITLE OF INVENTION: Requences and Antibodies Thereto
APPLICAMT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
ATTIE OF INVENTION AND ATTIES TO OCHOUTER: USA OF ATTIES TO OCHOUTER: IBM PC COMPATA:
MEDIUM TYPE: Floppy disk
COMPUTER: READBALE FRAM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION AND ATA:
APPLICATION WINBER: USA/08/724,394A
CLASSIFICATION STATE: USA/08/724,394A
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 35,136
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 35,136
REFERENCE/DOCKET NUMBER:
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STREET: 1225 Connecticut Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MAME/KEY: misc_feature
LOCATION: 1.3416
OTHER INFORMATION: /note- "cDNA 44"
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Search completed: June 16, 2003, 08:47:04 Job time : 42.9504 secs

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June 16, 2003, 03:58:29; Search time 188.731 Seconds (Without alignments) 6849.143 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                           2185239 seqs, 1125999159 residues
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Gapop 60.0 , Gapext 60.0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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AAI58784 ABL34086 ABL32478 ABL92305 AAL93064 AAI88702 AAI88891 AAI88891 AAIS7612 ABL67877 ABL67877 ABAS7396 ABAS7396 ABAS7396 ABAS7396	25241 25781 11100 6826 6826 6826 55114 6585 6585 103214 103214	K51610 D08380 C84349 L90182 ALIGNMENT	ID NO: dulator anti-H lmologi zheimer ; gene n; ss. r; R, F.
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44444444444444444		4.7 4.7 4.7 4.7	ed prote ted prote ted prote al, antilanglo nticonvu nticonvu li vulne dinate d dinate d d RI.  Al.  RR, Bl.  KP, Bl.  Moore P.
222222222222222222222222222222222222222		27 27 27 27 27 89 97 89 89	Ol-JUN-2001 (first entry) Human secreted protein cDNA Human; secreted protein; im dermatological; antinflamm vascular; anti-anglogenic; nootrople; anticonvulsant; antimLcrobial; vulnerary; v protein coordinate data; in Homo saplens. WO200121658-A1. 29-MAR-2001. 22-SEP-2000; 2000WO-US26013 24-SEP-1999; 99US-0155709 (HUMA-) HUMAN GENOME SCI IN Ni J, Baker KP, Birse CE, Lafleur DW, Moore PA, Olss Young PE, 'Wel P, Florence
110 111 112 113 114 116 116 117 117 118 118 118 119 119 119 119 119 119 119	440 440 440 440		Human Human derman vascu nootr antim prote Homo WO200 29-MA: 22-SE: 24-SE: (HUMA NI J, Lafler Young
0 0 0 0	0 000	REST AAFG XX XX	DT 01  XX  XX  XX  XX  XX  XX  XX  XX  XX

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The present sequence encodes one of 32 novel human secreted polypeptides.

The nucleic acid molecules and polypeptides they encode may be used in the nucleic acid molecules and treatment of diseases such as the prevention, diagnosis and treatment of diseases such as an immuno-deficiency virus (HIV) infections), hyperproliferative disorders (e.g. cancers and Gaucher's disease), cardiovascular diseases of Schmitter syndrome, Chapa's cardiomyopathy and coronary (e.g. Schmitter syndrome, Chapa's cardiomyopathy and coronary arteriosclerosis), angiogenic disorders (e.g. corneal graft neovascularisation and diabetic retinopathy), neurological disorders (e.g. Huntington's chorea, Alzheimer's diseases and parkinson's disease), infectious diseases and/or for promoting wound healing, regeneration and/or chemotaxis. The nucleic acid molecules may be used to produce the secreted polypeptides. They may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acid sequences in samples. The polypeptides may be used as antigens in the body control of antibodies and in assays to identify modulators of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rat sequence differentially expressed in response to a hepatotoxin #508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rat; ss; hepatotoxin; expressed sequence tag; EST; drug screening; differential expression; centrilobular necrosis; steatosis.
                                    Nucleic acids encoding 32 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease and diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 31; DB 22; Length 908;
Pred. No. 0.0039;
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100.0%; Pred. No. v...
... 0; Mismatches
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                                                                                                              Claim 1; Page 730; 890pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                            their expression and activity.
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2001US-298884P.
2001US-303459P.
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13-JUN-2001;
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Gaps

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predicting toxic effects of compounds or the progression of these toxic effects by determining the changes in gene expression in tissues or cells exposed to the toxin and comparing these to gene expression in
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                                                                                                                                                                                                                                           Query Match 5.1%; Score 29; DB 24; Length 569; Best Local Similarity 100.0%; Pred. No. 0.026; Matches 29; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                 Sequence 569 BP; 132 A; 98 C; 117 G; 222 T; 0 other;
                                      Claim 1; Seq ID No 508; 239pp; English.
                            unexposed tissues or cells -
WPI; 2002-241625/29.
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Human secreted protein gene 10 SEQ ID NO:20. AAF81796 standard; cDNA; 1926 BP 12-JUN-2001 (first entry) AAF81796; RESULT 3 g

antialzheimer; antiparkinsonian; antimicrobbal; vulnerary; gene therapy; immune disorder; hyperproliferative disorder; cardiovascular disease; cancer; angiogenic disorder; neurological disorder; infectious disease; wound healing; regeneration; chemotaxis; chromosome 20; ss. dermatological; immunosuppressive; antiinflammatory; anti-HIV; immunostimulant; cytostatic; cardiant; vascular; anti-angiogenic; ophthalmological; neuroprotectant; nootropic; anticonvulsant; vaccine; Human; secreted protein; diagnosis; immunomodulatory; antisclerotic;

Homo sapiens.

WO200112775-A2.

Castle AL, Elashoff MR;

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17-JAN-2001; 2001WO-US01354
                                                                                                                                02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
18-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      AMEB1787 to AAFB1817 encode the human secreted proteins given in AAB74733 to AAB74772. Human secreted proteins can have activities based on the tissues and cells they are expressed in. Example of activities include: CC immunomodulatory; antisclerotic; dermatological; immunosuppressive; antinfilammatory; antisclerotic; dermatological; immunosuppressive; cc antinfilammatory; anti-Hry; immunostimulant; cytostatic; cardiant; cardiant; antiablablames; antiparkinsonian; antimicrobial; and convulsant; antiablablames; antiparkinsonian; antimicrobial; and vaccine. Human secreted protein scan be used in gene therapy and cytostatic with inappropriate polypeptide expression; for example, NAM1 and proteins can be used in the prevention, diagnosis and treatment of diseases and PEP1 may be used to treat disorders associated with decreased conversion by rectifying mutations or deletions in a patients genome conversion by rectifying mutations or deletions in a patients genome conversion by rectifying mutations or deletions in a patients genome conversion by prevented, diagnosed and/or treated include immune disorders, and prepared in disorders, and disorders, conversion of the promoting wound healing, regeneration and /or chemotaxis. AAF81778 to the present incertion and include in the exemplification of the present incertion of the present and the present of the pr
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cytostatic; gene therapy; vaccine; metastasis; ss.
                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding 25 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease and diabetic retinopathy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:2122.
                                                                                                                                                                                                               Wei P, Baker KP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 5.1%; Score 29; DB 22; Length 1926; Best Local Similarity 100.0%; Pred. No. 0.021; Matches 29; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                    Soppet DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1926 BP; 519 A; 429 C; 430 G; 548 T; 0 other;
                                                                                                                                                                                                 Rosen CA, NI J, Florence KA, Fiscella M, Wei F
Birse CE, Young PE, Komatsoulis GA, Moore PA,
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                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 446; 485pp; English.
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                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC
                                                                 16-AUG-2000; 2000WO-US22325.
                                                                                                               99US-0149182.
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                                                                                                                                                                                                                                                              WPI; 2001-147550/15.
P-PSDB; AAB74742.
                                                                                                             17-AUG-1999;
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                       22-FEB-2001.
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Ruben SM;
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                                                                                                                                                                                                               Rosen CA, Barash SC,
                                                                                                                                                                                                                     WPI; 2001-483426/52.
P-PSDB; AAM84281.
        02-0CT-2000;
02-0CT-2000;
02-0CT-2000;
13-0CT-2000;
13-0CT-2000;
20-0CT-2000;
                                                                                                                                                                    5-DEC-2000;
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                                       20-OCT-2000;
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                                                                               08-NOV-2000;
                                                                                  NOV-2000;
                                     20-OCT-2000
                                                                                                                                                                                             08-DEC-2
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) anto acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and proteins and polynucleotides may be used to treat disorders associated with decreased example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome comparable of the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) cupplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting content (I) proteins and polynucleotides may be used to prevent, (I) proteins and polynucleotides may be used to prevent, (I) proteins and polynucleotides may be used to prevent, (I) proteins and polynucleotides may be used to prevent, (I) proteins and polynucleotides may be used to prevent, (I) proteins and polynucleotides may be used to prevent, (I) proteins and polynucleotides may be used to prevent, (I) proteins and polynucleotides may be used to prevent, (I) proteins and polynucleotides may be used to prevent, (I) proteins and polynucleotides may be used to prevent, (I) proteins and polynucleotides may be used to prevent, (I) proteins and polynucleotides may be used to prevent, (I) proteins and polynucleotides may be used to prevent, (I) proteins and polynucleotides may be used to prevent, (I) proteins and polynucleotides may be used to prevent, (I) proteins and polynucleotides may be used to prevent, (I) proteins and polynucleotides may be used to prevent, (I) proteins and polynucleotides may be used to prevent, (I) proteins and polynucleotides may be used to prevent, (I) proteins and polynucleotides may be used to prevent, (I) proteins and prevent manuely polynucleotides may be used to prevent.
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Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0%; Pred. No. 0.074;
Matches 28; Conservative 0; Mismatches 0; Indels
                                                                                                                      Claim 1; SEQ ID NO 2122; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 296 BP; 110 A; 66 C; 57 G; 61 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 CCCACGCGTCCGCCCACGCGTCCGCACA 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 cccacgcgTccGcccacGcGTCCGCACA 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human polynucleotide SEQ ID NO 7372.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . AAI87312 standard; cDNA; 401 BP.
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18-MAY-2000; 2000US-0577409.
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P-PSDB; AAO07381.
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us-10-090-035-3.rng

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The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy, The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, memantopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity information activity and may be useful in the diagnosis and/or treatment of cancer, leukaemla, nervous system disorders, arthritis and
                                                                                                                                                                        Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; secreted protein; gene therapy; protein therapy; cancer; weight; tumour; chromosome mapping; forensic; haematological disease; allergy; inflammation; cell proliferation; viral infection; wound healing; modulation; appetite; behaviour; food additive; preservative; ss.
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                                                                                                                                                                                                                                                               4.9%; Score 28; DB 22; Length 401;
100.0%; Pred. No. 0.07;
vative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                  Sequence 401 BP; 92 A; 110 C; 78 G; 121 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human secreted protein gene 14 clone HHEPT60.
                                                                                                                                                                                                                                                                                                                       2 CCCACGCGTCCGCCCACGCGTCCGCACA 29
                                                                                                                                                                                                                                                                                                                                      1 CCACGCGTCCGCCCACGCGTCCGCACA 28
                                                                                                                                                                                                                                                                                                                                                                                                                        AAX22224 standard; DNA; 532 BP.
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9705-0052873
9705-0052874
9705-0052874
9705-0053440
9705-0053441
9705-0055442
9705-0055724
9705-0055724
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Best Local Similarity 100.09
Matches 28; Conservative
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97US-0056359.
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Gaps

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The invention relates to nucleic acid sequences (AAX22211 to AAX22283) encoding human secreted proteins (AAY01831 to AAY01454). The secreted proteins (AAY01831 to AAY01454). The secreted colding human secreted proteins (AAY01831 to AAY01454). The secreted proteins are deposited with the ATCC under deposit number ATCC 209188, 209139, 209139 or 209114. Host cells containing vectors comprising the nucleic acid sequences are used for the recombinant expression of useful for preventing, treating or ameliorating medical conditions ergon by protein or gene therapy. Pathological conditions can be also diagnosed by determining the amount of the new polypeptides in a sample or by the sequences, or its fragments, are useful for chromosome identification conditions and mapping; as antisanse and triplex-forming therapeutics; in gene weight markers; to identify related sequences or specific acid weight markers; to identify related sequences or specific mRNA; in the preparation of oligomers and to raise anti-DNA antibodies. Antibodies are therapeutically to inhibit or activate particular polypeptides of disorders may be treated with the polynuclectide and conditions of disorders may be treated with the polynuclectide and allowy, inflammation, cancer or other forms of cell proliferation, viral conditate differentiation of embryonic stem cells, to modulate weight, concert or other forms of cell in wound healing, appetite, behaviour etc. and as food additive or preservative. The presents a gene encoding a human secreted protein.
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                                                                                                                                                             New nucleic acids encoding secreted human proteins - potentially useful for treating and diagnosing diseases and identifying specific
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4.9%; Score 28; DB 20; Length 532;
Best Local Similarity 100.0%; Pred. No. 0.066;
Matches 28; Conservative 0; Mismatches 0; Indels
Duan R, Feng P, Ferrie AM, Florence KA, Fouad J;
Greene JM, Hu J, Ni J, Rosen CA, Ruben SM, Young PE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 532 BP; 113 A; 146 C; 126 G; 147 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human ovarian antigen HSPSI74 cDNA, SEQ ID NO:187.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 4; Page 176; 251pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABQ54307 standard; cDNA; 1592 BP.
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                                                                                            WPI; 1999-132234/11.
P-PSDB; AAY01396.
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03-JAN-2002

Birse CE,

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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM36642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynuclectides are useful ingene therapy. A composition containing a polypeptide or polynuclectide or polynuclectide or the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as lacalised neuropathies and central nervous system diseases, and the atlatifies and shy-brager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence data for this patent did not form part of the printed
                                        Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Liu C, Asundi V, Chen R, Ma Y, Wang Z, Wehrman T, Xu C, Xue AJ, Zhou P, Goodrich R, Drmanac RT;
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Human polynucleotide SEQ ID NO 147.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0552317.
2000US-0598042.
2000US-0620312.
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2000US-0693036
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P-PSDB; AAM38788.
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                                                                                                                                                                                                                                                                                           WO200153312-A1.
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                                                                                                                                                                                           leukaemia; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local S...
28;
                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-JUL-2000;
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Best Local Si
Matches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tang YT,
Wang J, W
Zhao QA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAK51691
          Ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to 2175 novel human ovarian antigens (ABP41054-CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also cnompasses polypeptides 90% identical and polynucleotides 95% identical corporations and host cells comprising human ovarian antigen to the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen polynucleotides and polypeptides in diagnosing, creating, prognosing or preventing various ovary and/or breast cancer, and disorders. Such conditions include ovarian cancer and breast cancer, and clasorders (e.g., infertility, disorders of pregnancy, anovulation, disorders, infertility, disorders of pregnancy, anovulation, disorders, infertility, disorders of pregnancy, anovulation, collocations, infilammatory conditions (e.g., mastitis, oophoritis and varianties), immune disorders (e.g., congenital and acquired clasorders, autoimmune ophoritis, systemic lupus erythematosus), immunedificiencies, autoimmune ophoritis, systemic lupus erythematosus, immunodeficiencies, autoimmune ophoritis, systemic lupus erythematosus, collocatiates disorders, neurological disorders, gastrointestinal disorders and urinary system disorders, ovarian antigen polypeptides and complementation of individuals and in screening for compounds which modulate ovarian antigen expression or activity. The polynucleotides may he used as food additives or to prepare antibodies collentification of individuals and in forensic analysis, and the individuals and in disease diagnosis, drug targeting and phenotyping. The present securing and phenotyping of the function of function of the function of function of functions of the function of functions o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ilarity 100.0%; Pred. No. 0.0
Conservative 0; Mismatches
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100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID No 187; 2922pp; English.
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                                                                                                                                                     07-JUN-2001; 2001WO-US18569.
                                                                                                                                                                                                         07-JUN-2000; 2000US-209467P.
                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME
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les 28; Conserv
                                                                                                                                                                                                                                                                                                              Rosen CA;
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                                                      WO200200677-A1.
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Wang

Ren F, Wang J;

Qian XB, Yang Y,

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Gaps

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AAK51691;

SX B

(first entry)

22-OCT-2001

AAI57944;

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RESULT 8 AAI57944

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Query Match Matches 7

us-10-090-035-3.rng

nootropic; immunosuppressant; cytostatic;

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peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries \cdot
                                                                                                Human polynucleotide SEQ ID NO 987.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-DEC-2000; 2000WO-US34263
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29-NOV-2000; 2000US-0727344
                                22-OCT-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                            WO200153312-A1.
                                                                                                                                                                                                                                                                                                         leukaemia; ss
                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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14-SEP-2000;
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Zhao QA,
                                NAME OF STREET O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and may activity, and may and elasticity in the contraction of 
                                                                                                                                                Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ma Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAW80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y,
Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang 2W;
Xue AJ, Yang Y, Wejhrman T, Goodrich R;
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100.0%; Pred. No. 0.044;
Live 0: Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 1115-1120; 6221pp; English.
                                                                                      Human polynucleotide SEQ ID NO 236.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-JUN-2000; 2000US-0598075.
19-JUL-2000; 2000US-0620325.
01-SEP-2000; 2000US-0654936.
15-SEP-2000; 2000US-0663561.
20-OCT-2000; 2000US-0693325.
30-NOV-2000; 2000US-0728422.
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2000US-0560875.
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                            06-NOV-2001 (first entry)
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P-PSDB; AAM78558.
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                                                                                                                                                                                                                                                                                                         Homo sapiens.
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Ren F, Wang D; Zhang J;

Qian XB, Yang Y,

Liu C, Asundi V, Chen R, Ma Y,
Wang Z, Wehrman T, Xu C, Xue AJ,
Zhou P, Goodrich R, Drmanac RT;

2000US-0620312. 2000US-0653450. 2000US-0662191.

2000US-0552317. 2000US-0598042.

2000US-0488725

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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous localised neuropathies and central nervous system diseases, such as Lateral sclerosis, and shorager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, and thrombolytic activity, chemotactic/chemokinetic activity, haemostatic assays for receptor activity, arthritis and inflammation, leukaemias and ch. S disorders.
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4.9%; Score 28; DB 22; Length 4929;
Best Local Similarity 100.0%; Pred. No. 0.044;
Matches 28; Conservative 0; Mismatches 0; Indels (
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Claim 1; SEQ ID NO 987; 10078pp; English.
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ABL34086/c
ID ABL34086 standard; DNA; 5928
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Gaps

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Local Similarity 100.

Matches

ð g AAI58784 standard; cDNA; 4929 BP

AAI58784;

RESULT 10
AAI58784
ID AAI58
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AC AAI58:

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WO200181622-A2.
                                                                                               WO200200928-A2.
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                                        gene; ds.
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ABL92305/c
                                                                       Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute mysloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; Immune system disease; cytosine methylation; antiasthmatic;
antiarteriosclerotic; antianaemic; cytostatic; nootropic;
neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
                                                                                                  Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirinematic; antiarthritic; antidiabetic; antipsoriatic; antinflammatory; cancer; eye disease; arteriosclerosis; anaeute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy: neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
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                                                                          Human immune system associated gene SEQ ID NO: 2059.
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0.043;
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01-SEP-2000; 2000DE-1043826
                                                                                                                                                                                                                                                                                                                               02-JUL-2001; 2001WO-EP07537
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                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytosine methylation
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nes 28; Conserv
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                       ABL34086;
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chemically treated DNA repair gene fragment complementary to#57.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6593 BP; 1732 A; 121 C; 1448 G; 3292 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 451; 32pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
                                                                                                                                                                                                                                                                                                                                                                         02-JUL-2001; 2001WO-EP07537
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Best Local Similarity 100.0
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytosine methylation
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The present invention relates to oligonucleotides encoding polymorphic variants of proteins related to amylases, amyloid proteins, angiopoletin, apoptosis related proteins, cadherin, cytlin, polymerses, oncogenes, histones, kinases, colony stimulating factors, complement related proteins, cytochromes, kinesins, cytokines, interferons, interleukins, complement related protein coupled receptors and thioseterases. The present sequence is one such oligonucleotides and the peptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autolumune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus erythromatosus and Grave's diseases), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, leukaemia), diseases of the nervous system and an infection of pathogenic
                                                                                                                                                                                                                                                                                                Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; colon cancer; colon cancer antigen; diagnosis; detection; colorectal carcinoma; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human colon cancer antigen encoding cDNA SEQ ID NO:120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 51 BP; 11 A; 1 C; 3 G; 36 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Pred. No. 0.7 tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            548 AATACTAAAAAAAAAAAAAAAAAA 574
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAH33064 standard; cDNA; 233
                                                                              28-DEC-1999; 99US-0173419.
27-DEC-2000; 2000US-0173419.
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                                   28-DEC-2000; 2000WO-US35498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0157137.
99US-0163280.
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Matches 27; Conservative
                                                                                                                                                                                                     Shimkets RA, Leach M;
                                                                                                                                                        (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                     WPI; 2001-465210/50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to nucleic acids containing a sequence of at least 18 nucleotides of chemically treated DNA of genes associated with DNA repair, and their complements. The invention also relates to nucleic acids comprising at least 18 base pairs of the chemically pretreated DNA of genes associated with DNA repair selected from PMS2L1, PMS2L12, PMS2L3, PMS2L3, PMS2L5, PMS2L5, MGMT, MSH2, NUDT1, TDG, INPPL1, RFG4, DDIT1L, FANCB, or XRCG8, Nucleic acids of the invention and related oligomers, are useful for diagnosis of diseases associated with gene repair, specifically ataxia telanglectasia, aging, Bloom's syndrome, Cockayne syndrome, Nijmegen breakage syndrome or Werner syndrome, Immunodeficiency, trichthiodystrophy, Fanconi's anaemia, solid tumours and cancer, particularly by determining status of cytosine methylation and related and/or by detecting single-nucleotide polymorphisms. Determination of individual methylation patterns may allow development of individualised theraples. The sequences given in records ABL92192-ABL92335 represent consisted with DNA
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                                                                                                                                                                                                                                                               New nucleic acid derived from genes associated with DNA repair, useful for diagnosis, e.g. of ataxia telanglectasia, by determination of cytosine methylation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence data for this patent is not represented in the ification, but is based on sequence information supplied by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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Pred. No. 0.036;
0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13919 BP; 3717 A; 296 C; 3349 G; 6557 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 114; 25pp + sequence listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.9%; Score ____ 100.0%; Pred. No. 0.0st
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and their complements.
                    2000DE-1019173
2000DE-1032529
                                                                    01-SEP-2000; 2000DE-1043826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAL30125 standard; DNA; 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28; Conservative
                                                                                                                                                                  Olek A, Piepenbrock C,
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                                                                                                                  (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                  WPI; 2002-034446/04.
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Matches 28; Conserv
06-APR-2000;
                         J-APR-2000;
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AAL30125;

RESULT 14 AAL30125/c

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Gaps

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0; Indels

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WPI; 2001-235357/24.
P-PSDB; AAG73633.
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Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -

Claim 1; Page 2294; 9803pp; English

cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing in a patient's genome that affect the activity of P by expressing hadditionally. N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and AAB77789 represent sequences used in the exemplification of the M.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922. AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon

Sequence 233 BP; 116 A; 37 C; 40 G; 40 T; 0 other;

ö Score 27; DB 22; Length 233; 0; Indels Pred. No. 0.19; 4.7%; Scor. 100.0%; Pred. No. v... 0; Mismatches 1 ACCCACGCGTCCGCCCACGCGTCCGCA 27 27; Conservative Query Match Best Local Similarity Matches 27; Conserva à

Gaps

Search completed: June 16, 2003, 06:54:05 Job time: 192.231 secs

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OM nucleic

Run on:

Word size :

Searched:

Sequence:

Database :

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Sequence 18, Appl
Sequence 674, App
Sequence 774, App
Sequence 7993, Ap
Sequence 2551, Ap
Sequence 2551, Ap
Sequence 265, App
Sequence 265, App
Sequence 16114, A
Sequence 76, Appl
Sequence 69, Appl
Sequence 69, Appl
Sequence 16810, A
Sequence 16810, A
Sequence 16811, A
Sequence 16811, A
Sequence 1681, A
Sequence 1681, A
Sequence 1681, A
Sequence 1651, A
Sequence 7, Appl
Sequence 7, Appl
Sequence 7, Appl
Sequence 16, Appl
Sequence 1355, A
Sequence 66, Appl
Sequence 66, Appl
Sequence 66, Appl
Sequence 61, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:

APPLICANT: SImmons, Carl R.

TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible
TITLE OF INVENTION: Proteins and Uses Thereof
FILE REFERENCE: 35718/242990
CURRENT APPLICATION NUMBER: US/10/090,035
CURRENT APPLICATION NUMBER: 05/202
PRIOR PILING DATE: 2002-02-28
PRIOR FILING DATE: 02/28/2001
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 574
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Best Local Similarity 100.0%; Pred. No. 2.5e-278;
Matches 574; Conservative 0; Mismatches 0;
9 US-10-105-891-28
9 US-10-098-841-148
9 US-10-037-270-1674
9 US-09-918-995-7993
9 US-09-918-995-7993
9 US-09-925-299-265
10 US-09-918-995-2984
9 US-09-918-995-2984
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2. C902_6 / ptodata/2/pubpna/USO6_NEW_PUB. seq:*

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3. C903_6 / ptodata/2/pubpna/USO6_NEW_PUB. seq:*

5. C903_6 / ptodata/2/pubpna/USO8_NEW_PUB. seq:*

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12. C903_6 / ptodata/2/pubpna/USO9_NEW_PUB. seq:*

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TITLE OF INVENTION: NUCLEIC ACIDS Encoding Defense Inducible
TITLE OF INVENTION: Proteins and Uses Thereof
FILE REFERENCE: 35718/242990
CURRENT PILITIG DATE: 2002-02-28
CURRENT FILING DATE: 2002-02-28
PRIOR PILICATION NUMBER: 60/272,227
PRIOR FILING DATE: 02/28/2001
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1.
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Pred. No. 2.3e-147;
0; Mismatches 3;
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Patent No. US20020170089A1
GENERAL INFORMATION:
APPLICANT: Simmons, Carl R.
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Conservative 0
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; Sequence 5, Application US/10090035
; Patent No. US20020170089A1
; GENERAL INFORMATION:
    APPLICANT: Simmons, Carl R.
    TITLE OF INVENTION: Proteins and Uses Thereof
    TITLE OF INVENTION: Proteins and Uses Thereof
    TITLE OF INVENTION: Proteins and Uses Thereof
    CURRENT APPLICATION UNMER: US/10/090,035
    CURRENT FILING DATE: 2002-02-28
    PRIOR PPLICATION NUMBER: 60/272,227
    PRIOR PPLICATION NUMBER: 60/272,227
    PRIOR FILING DATE: 02/28/2001
    NUMBER OF SEQ ID NOS: 25
    SOFTWARE: FastSEQ for Windows Version 4.0
    SEQ ID NO 5
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244 ACCACCACCACCATGGTCACCACGGCGCCACGGCTTCGTGGTGCGCGAGACCAGGG 303
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                                                                                                                                                                                                                                     Gaps
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Fatent No. US20020170089A1
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible
TITLE OF INVENTION: Proteins and Uses Thereof
TITLE OF INVENTION: Proteins and Uses Thereof
CURRENT FILING DATE: 2002-02-28
FRICE REPERENCE: 35718/742990
CURRENT APPLICATION NUMBER: 05/10/090,035
FRICE REPERENCE: 30728/2901
FRICE REPERENCE: 2002-02-28
FRICE RELING DATE: 02/28/2001
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 524
                                                                                                                                                                                                    Length 580;
                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                               31.0%; Score 178; DB 9;
99.1%; Pred. No. 1.3e-79;
tive 0; Mismatches 3
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24.2%; Score 139; DB 9;
Best Local Similarity 99.5%; Pred. No. 4.7e-60;
Matches 189; Conservative 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      544 TCGTAATACTAAAAAAAAAAAAAAAAAAA 574
            NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 580
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LOCATION: (57)...(338)
NAME/KEY: misc_feature
LOCATION: (1)...(524)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                           Query Match
Best Local Similarity 99.1'
Matches 328; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Triticum aestivum
                                                                                                                            ; NAME/KEY: CDS
; LOCATION: (99)...(380)
US-10-090-035-7
                                                                             TYPE: DNA
ORGANISM: Zea mays
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450 TIGITCAGGGTCATCGTACTTGGCTATCGTACGTGCACGCACTCAGCTCCTGTACGAATT 509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 GTGGCCCGGCCGGCTTCGGCCGCCACGGCGGCGCGTCCAGCAGCACGTCAAGGAG 160
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Sequence 9, Application US/10090035

Sequence 9, Application US/10090035

Sequence 9, Application US/10090035

Sequence 9, Application US/10090035

TILE OF INVENTION: Uncleic Acids Encoding Defense Inducible TILE OF INVENTION: Nucleic Acids Encoding Defense Inducible FILE OF INVENTION: Nucleic Acids Encoding Defense Inducible FILE REFERENCE: 35718/242990

CURRENT FILING DATE: 202-02-28

PRIOR FILING DATE: 002-02-28

PRIOR FILING DATE: 002-02-28

SOFTWARE: FASTERO FOR Windows Version 4.0

SEQ ID NOS: 25

SOFTWARE: FASTERO FOR Windows Version 4.0
                                                                                              510 ACGACAATAAGCTCGTGACCTGAATAAAACTTCTTCGTAATACTAA 555
                                                                                                                  Length 529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/10090035
Patent No. US20020170089A1
GENERAL INC. US20020170089A1
GENERAL INC. US20020170089A1
GENERAL INCOMMATION: Carl R.
TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible FILE REFERENCE: 35748/242990
CURRENT APPLICATION NUMBER: US/10/090,035
CURRENT APPLICATION NUMBER: 60/272,227
PRIOR FILING DATE: 02/28/2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 194; DB 9;
Pred. No. 1.2e-87;
0; Mismatches 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.8%;
al Similarity 99.3%;
294; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (53);...(331)
US-10-090-035-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 294; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Zea mays
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US-10-090-035-7
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NUMBER OF SEQ ID NOS: 25 SOFTWARE: FastSEQ for Windows Version 4.0
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 591
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 15, Application US/10090035 Patent No. US20020170089A1
                                                                                                                                 ; LOCATION: (1)...(348); OTHER INFORMATION: n = A,T,C or G US-10-090-035-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - A,T,C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS
LOCATION: (61)...(333)
NAME/KEY: misc_feature
LOCATION: (1)...(591)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Oryza sativa
                                  TYPE: DNA
ORGANISM: Oryza sativa
                                                                                 NAME/KEY: CDS
LOCATION: (52)...(348)
NAME/KEY: misc_feature
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US-10-090-035-21
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SEC ID NO 13
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                                                                  FEATURE
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                                                      ACGICGICAAGGAGAAGIICGAGGAGGICGACACGGICICACGCGCGGCGCCAACCACC 249
                                                                                                                          4 CACAGACACCAAGCGTCGGCACCAATGGCTTACTACCAGGAGGGGGACTACTGCTCGG 93
 31 CACAGACACACCAAGCGTCGGCACCAATGGCTTACTACCAGGAGGTGGACTACTGCTCGG 90
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| OTHER INFORMATION: Incyte ID No. US20020013958A1 700161180H1
| NAME/KEY: unsure
| LOCATION: 125-146, 202
| OTHER INFORMATION: a, t, c, g, or other
| US-09-923-876-2788
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APPLICANT: Simmons,
TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible
TITLE OF INVENTION: Proteins and Uses Thereof
FILE REFERENCE: 35718/242390
CURRENT APPLICATION NUMBER: US/10/090,035
CURRENT FILLING DATE: 2002-02-28
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100.0%; Pred. No. 6.2e-36;
tive 0; Mismatches 0; Indels
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PRIOR APPLICATION NUMBER: 60/272,227
PRIOR FILING DATE: 02/28/2001
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                Sequence 2788, Application US/09923876
Patent No. US20020013958A1
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; Sequence 13, Application US/10090035
; Patent No. US20020170089A1
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Best Local Similarity 100.(
Matches 91; Conservative
                                                                                                                                                                                                    211 ACCACCACCA 220
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ORGANISM: Zea màys
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Sequence 21, Application US/10090035
Sequence 21, Application US/10090035
Sequence 21, Application US/10090035
GENERAL INFORMATION:
APPLICARY: Simmons, Carl R.
TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible TITLE OF INVENTION: Proteins and Uses Thereof FILE REFERENCE: 35718/242990
CURRENT APPLICATION NUMBER: US/10/090,035
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 60/272,227
NUMBER OF FILING DATE: 02/28/2001
                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Simmons, Carl R.
TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible TITLE OF INVENTION: Proteins and Uses Thereof FILE REPERROCE: 35718/242990 CURRENT APPLICATION NUMBER: US/10/090,035 CURRENT FILING DATE: 2002-02-28 PRIOR APPLICATION NUMBER: 60/272,227 PRIOR FILING DATE: 02/28/2001
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Ouery Match
Best Local Similarity 100.0%; Pred. No. 2.3e-12;
Matches 44; Conservative 0; Mismatches 0; Indels
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TILLE OF INVENTION: 32 Human secreted proteins
FILE REFRENCE: P2044P1
CURRENT APPLICATION NUMBER: US/09/800,729
CURRENT FILING DATE: 2001-03-08
FRIOR APPLICATION NUMBER: PCT/US00/26013
PRIOR APPLICATION NUMBER: 60/155,709
PRIOR FILING DATE: 1999-09-24
NUMBER FILING DATE: 1999-09-24
NUMBER FO SEQ ID NOS: 217
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
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5.9%; Score 34; DB 9; L.
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 34; Conservative 0; Mismatches 0;
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7e-06;
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OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (891)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (896)
COTHER INFORMATION: n equals a,t,g, or c
US-09-800-729-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 17655, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 25, Application US/09800729 Patent No. US20020068319A1
                                                                                                                   ; LOCATION: (1)...(584)
; OTHER INFORMATION: n = A,T,C or G
US-10-090-035-23
                                                LOCATION: (46)...(321)
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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US-10-090-035-19
Sequence 19, Application US/10090035
TITLE OF UNVENTION:
TITLE OF INVENTION:
FILE REPERENCE: 35718/242990
CURRENT APPLICATION NUMBER: US/10/090,035
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 05/272,227
PRIOR APPLICATION NUMBER: 05/272,227
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 19
LENGER 1584
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Fatent No. US20020170089A1
GENERAL INFORMATION:
TERE TINFORMATION:
TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible
TITLE OF INVENTION: Proteins and Uses Thereof
FILE REFERENCE: 35718/242990
CURRENT FILING DATE: 2002-02-28
FRIOR APPLICATION NUMBER: 60/272,227
PRIOR APPLICATION NUMBER: 60/272,227
FRIOR FILING DATE: 02/28/2001
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 584
                                                                                                                                                                                                                                                               Ouery Match 5.9%; Score 34; DB 9; Length 436; Best Local Similarity 100.0%; Pred. No. 2.3e-07; Matches 34; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 34; Conservative 0; Mismatches 0;
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LOCATION: (46)...(321)
NAME/KEY: misc_feature
LOCATION: (1)...(584)
OTHER INFORMATION: n = A,T,C or G
                                                              ORGANISM: Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Triticum aestivum
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ORGANISM: Triticum aestivum
FEATURE:
                                                                                                                          ; NAME/KEY: CDS
; LOCATION: (54)...(326)
US-10-090-035-21
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LENGTH: 436
                                  TYPE: DNA
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                                                                                                                                                                                                                       Length 538;
                                                                                                                                                                                                                                                                         0; Indels
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TITLE OF INVENTION: MOLECULAR TOXICOLOGY MODELING
FILE REFERENCE: 44921-5038-US
CURRENT APPLICATION NUMBER: US/09/917,800A
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR FILING DATE: 2000-07-31
PRIOR PELING DATE: 2000-11-02
PRIOR FILING DATE: 2001-05-11
PRIOR FILING DATE: 2001-05-11
PRIOR PLING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR PLING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: US 60/292,336
                                                                                                                                                                                                                       Query Match 5.1%; Score 29; DB 9; L Best Local Similarity 100.0%; Pred. No. 7.4e-05; Matches 29; Conservative 0; Mismatches 0;
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PRIOR APPLICATION NUMBER: US 60/298,884
PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/303,459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 2001-05-22 APPLICATION NUMBER: US 60/295,798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 2001-06-06
APPLICATION NUMBER: US 60/297,457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 508, Application US/09917800A Patent No. US20020119462A1 GENERAL INFORMATION: APPLICANT: Mendrick, Donna
                                                                                                NAME/KEY: misc_feature

| LOCATION: (1)...(538)

| OTHER INFORMATION: n = A,T,C or G

US-09-918-995-17655
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ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene Logic, Inc.
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 508
LENGTH: 569
LENGTH: 538
TYPE: DNA
ORGANISM: Homo sapiens
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Gaps Ouery Match
Best Local Similarity 100.0%; Pred. No. 7.4e-05;
Matches 29; Conservative 0; Mismatches 0; Indels

ò g Search completed: June 16, 2003, 10:24:26 Job time: 129.198 secs

RNOSEQ6C0

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BOG19337 RNOSEGGEI
BOG19383 RNOSEGGEI
BOG19380 RNOSEG7B0
BGG40383 MEST12-H1.
BM501439 PACO00000
BM502302 94502E06
BE025302 94502E06
AM787314 945013001
AM787314 945013001
AM787314 945013001
AM7867314 945013001
AM786731 94502E06
AM288055 707005E07
BM530859 945007B05
BED12964 945027B05
BM8875 707005E07
BM530859 4717£10.7
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BM530859 4717£10.7
BM15431 4789391.9
BM154314 4783311.9
BM154314 643311.9
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BM15431864 318253
AM781564 318253
BM50859705 8035909.7
BEC59705 8035909.7
BF777697 NXSL 073
BM508531 U£65604.9
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BM156431 U£65604.9
BM156721 U£65604.9
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AW787732 MY87732.1 GI:7844510
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1 (bases 1 to 500)
Walbot,V.
Walbot,V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Maize mc..
University
Unpublished (1999)
Contact: Malbot V
Contact: Malbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: Walbot@stanford.edu
Plate: 945002 row: E column: 06.
Location/Qualifiers
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                                                       AA979839
BM501439
AW787315
BE025302
A1964534
AW787314
AR855425
A1964458
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AW289056
BE025303
BE025303
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BM88875
BM885464
BM5308594
BM154314
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KEYWORDS
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AW787732
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TITLE
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AW28876 707009E07
BE129897 945032C12
AW331212 707049E04
AY104409 Zea mays
BQ619167 RNOSEQ4E0
                                                  June 16, 2003, 05:14:00; Search time 1370.39 Seconds (without alignments) 7989.092 Million cell updates/sec
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                                                                                                          Description
                                                                                                                                                                                               32308132
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                      16154066 segs, 8097743376 residues
                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                OM nucleic - nucleic search, using sw model
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AW288876
BE129897
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Maximum DB seq length: 200000000
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em_estom:*
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Result

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107
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SOURCE
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Zea mays
Lea mays
Lea mays
Lea mays
Stracheophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; PACC
clade; Panicoldeae; Andropogoneae; Zea.
1 (bases 1 to 524)
                                                                 /note="Organ: tassel, kernal, silk, husk, root, leaf;
Vector: pGAD10: Site_1: ECORI; cDNA library from fully
differentiated maize tissues from an active Mutator plant.
Tissue ratio is 4:2:1:1:1:1 (tassel, kernel, silk, husk,
root, leaf). Unidirectionally cloned. New library number
given to library 707 for additional sequencing."
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/db_xref="taxon:4577"
/db_xref="taxon:4577"
/clone_lib="945 - Mixed adult tissues from Walbot lab,
/clone_lib="945 - Mixed adult tissues from Walbot lab,
/clone_lib="945 - Mixed adult tissues from Walbot lab,
                                     silk, husk, root, leaf"
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                                     /tissue_type="tassel, kernal,
/dev_stage="fully-grown"
/lab_host="DH10B"
                                                                                                                                                              Score 308; DB Pred. No. 0; Mismatches
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Department of Biological Sciences
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mays cDNA, mRNA sequence.
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                                                                                                                                                               tch 45.6%;
al Similarity 99.3%;
458; Conservative
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ORIGIN
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AW288876
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Sea mays sea mays sea mays viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
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Vector: pGAD10; Site_1: ECORI; cDNA library from fully
differentiated malze tissues from an active Mutator
plant. Tissue ratio is 4/2/1/1/1/1 (tassel, kernel, silk,
plant. Toot, leaf). Unidirectionally cloned."
                                                                                                                                        (SK
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/db_xref="taxon:4577"
/clone_lib="707 - Mixed adult tissues from Walbot lab
                                                                                                                                                                /tissue_type="tassel, kernel, silk, husk, root, leaf"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       465 bp mRNA linear EST 945032C12.X1 945 - Mixed adult tissues from Walbot lab, EST 2ca mays cDNA, mRNA sequence.
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                                                                                                                                                                                                                                                                                                             Score 305; DB 10; Length 524;
Pred. No. 0;
0; Mismatches 3; Indels (
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Stanford University
B55 California Ave, Palo Alto, CP
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 770/009 row: E column: 07
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                  cch 45.1%;
al Similarity 99.3%;
455; Conservative (
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bunaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 523)
Walbot, V.
Maize ESTs from various cDNA libraries sequenced at Stanford
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/clone_lib="707 - Mixed adult tissues from Walbot lab (SK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="tassel, kernel, silk, husk, root, leaf"
/dev_stage="adult"
/lab_host="bH10B"
/note="Organ: tassel, kernel, silk, husk, root, leaf;
/note="Organ: tassel, kernel, silk, husk, root, leaf;
Vector: pGAD10; Site_1: EcoR1; cDNA library from fully
differentiated maize tissues from an active Mutator
plant. Tissue ratio is 4/2/1/1/1/1 (tassel, kernel, silk,
husk, root, leaf). Unidirectionally cloned."
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                                                                                                                                                                                                                                                                                                             Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, US,
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 707049 row: E column: 04.
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    .523
    /organism="Zea mays"
    /cultivar="W23"

                                                                                                                                                 Zea mays
Eukaryota; Viridiplantae;
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11 Similarity 99.2%;
46%; Conservative
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Vector: pGAD10; Site_1: EcoR1; cDNA library from fully
Vector: pGAD10; Site_1: EcoR1; cDNA library from fully
fisher ratio is 4:2:1::1:1 (tassel, kernel, silk, husk,
root, leaf). Unidirectionally cloned. New library number
given to library 707 for additional sequencing."
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/clone_lib="945 - Mixed adult tissues from Walbot lab, state as 707 (St)"
/tissue_type="tasse1, kernal, silk, husk, root, leaf" /dev_stage="fully-grown"
/lab_nost="DHIOB"
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                                   Walbot, V.
Maize ESTs from various cDNA libraries sequenced
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                                                                                             Unpublished (1999)
Contact: Walbot V
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Stanford University Palo Alto, CA 94304, USA
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Llarity 99.3%; Pred. No. 0;
Conservative 0; Mismatches
Panicoideae; Andropogoneae;
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/organism="Zea mays"
/cultivar="W23"
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nes 429; Conserv
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/ Organism="zea mays"
/ Organism="zea mays"
/ Ab_xref="Maizon:4577"
/ Clone="PCO124784"
/ Clone="PCO124784"
/ Clone="this sequence is part of a project of EST note="this sequence is part of a project of bublic assemblies resulting from the appliation of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize
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                                                                                    HTC 25-MAY-2002
                                                                                                                                                                     Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Zea.
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Anahaey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design
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Direct Submission
Submitted (25-APR-2002) Maize Mapping Project, University
Missouri, Columbia, MO 65211, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 261; DB 11; Length 553;
Pred. No. 0;
0; Mismatches 1; Indels (
                                                                                      linear
                                                                                      mRNA
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Zea mays PC0124784 mRNA sequence.
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                                                                                                                          AY104409.1 GI:21207487
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Best Local Similarity 99.7%;
Matches 311; Conservative
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Unpublished (2002)
2 (bases 1 to 553)
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Bukaryophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.

El (Masses It o 648)

Wang H. and Bohnert, H.J.
Genomics of plant stress tolerance
Unpublished (2002)
Unpublished (2002)
University of Illinois
University of Illinois
Il201 W. Gregory Dr., Urbana, IL 61801, USA
Tel: 217265443
Email: bohnertlab@life.uluc.edu.
Location/Qualifiers
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RNOSEQ4E05_SK.abl Salt stressed Zea mays roots cDNA library Zea
mays cDNA clone RNOSEQ4E05_SK.abl similar to No homology, mRNA
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/clone="RxNSEQ&EOS_SK.abl"
/clone_lib="Salt stressed Zea mays
/tissue_type="Roots"
/dev_stage="2 weeks old"
/note="Vector: pBluescript SK+; St
mM NaCl"
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Best Local Similarity 99.7
Matches 311; Conservative
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoldeae; Andropogoneae; Zea.
                                                                                                                                                        Email: bohnertlab@life.uiuc.edu.
Location/Qualifiers
1. .648
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RNOSEOGE12_SK.abl Salt stressed Zea mays roots cDNA library Zea
mays cDNA clone RNOSEQ6E12_SK.abl similar to No homology, mRNA
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99.7%; Pred. No. 0;
tive 0; Mismatches 1; Indels
                            1 (bases 1 to 648)
Wang, H. and Bohnert, H.J.
Genomics of plant stress tolerance
Unpublished (2002)
Contact: Mark Fredricksen
Department of Plant Biology
University of Illinois
1201 W. Gregory Dr., Urbana, IL 61801, USA
              Panicoideae; Andropogoneae; Zea.
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Wang, H. and Bohnert, H.J.
Genomics of plant stress tolerance
(Unpublished (2002)
Contact: Mark Fredricksen
Department of Plant Biology
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1 (bases 1 to 648)
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Genomics of plant stress tolerance
Unpublished (2002)
Contact: Mark Fredricksen
Department of Plant Biology
University of Illinois
1201 W. Gregory Dr., Urbana, IL 61801, USA
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/note="Roots"
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mays cDNA clone RNOSECGEDOL_SK.abl similar to No homology, mRNA
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38.6%; Score 261; DB 14; Length 648;
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Matches 311; Conservative 0; Mismatches 1; Indels (
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Zea mays
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/dev_stage="2 weeks old"
/note="Vector: pBluescript SK+; Stressed 24 hours at 150
mM NaC1"
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University of Illinois
1201 W. Gregory Dr., Urbana, IL 61801, USA
Tel: 2172655473
Email: bohnertlab@life.uiuc.edu.
Location/Qualifiers
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Wang H. and Bohnert, H.J.
Genomics of plant stress tolerance
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Mark Fredricksen
Department of Plant Biology
University of Illinois
1201 W. Gregory Dr., Urbana, IL 61
Tel: 2172655473
Email: bohnertlab@life.uluc.edu.
                                                                                                                                                                                                              Score 261; Pred. No. 0;
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Location/Qualifiers
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/organism="Zea mays"
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Best Local Similarity 99.7%;
Matches 311; Conservative
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Zea.

(Dases 1 to 648)

Wang, H. and Bohnert, H.J.

Genomics of plant stress tolerance
Unpublished (2002)

Contact: Mark Fredricksen
Department of Plant Biology
University of Illinois
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/db_xref="taxon:4577"
/clone="RNOSE07B02_SK.abl"
/clone_lib="salt stressed Zea mays roots cDNA library"
/tissue="Roots"
/dev_stage="2 weeks old"
/dev_stage="2 weeks old"
/note="Vector: pBluescript SK+; Stressed 24 hours at 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .648
/organism="Zea mays"
/db_xxef="taxon:4577"
/clone="RMOSEQ7B09_SK.abl"
/clone=lib="Salt stressed Zea mays roots cDNA library"
/tissue_type="%cots"
/dev_stage="2 weeks old"
/note="Vector: pBluescript SK+; Stressed 24 hours at 1"
mM NaC1"
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Tel: 217855473
Email: bohnertlab@life.uiuc.edu.
Location/Qualifiers
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                                                                                                                                                                                                 Query Match 38.6%;
Best Local Similarity 99.7%;
Matches 311; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 193 c
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GI:3157217
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Best Local Similarity 99.7'
Matches 306; Conservative
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AA979839
AA979839.1
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Zea mays
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ORIGIN
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KEYWORDS
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AA979839
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TITLE
JOURNAL
COMMENT
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MEST12-H11.T7-1 ISUM4-TN Zea mays CDNA clone MEST12-H11 5', mRNA
                                                                                                                                             417 CCTTATGTATGTCTGTGGTTGACTGGTTGTGCAGGGTCATCGTACTTGGCTATCGTACGT 476
                                                                                                                                                                                                                                         Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 550)

Qlu,F., Cui,F., Guo,L., Ashlock,D.A, Wen,T.J. and Schnable,P.S. Expressed Sequence Tags from B73 Maize Seedlings and Silks Unpublished (2001)

On May 25, 2001 this sequence version replaced gi:14206705.
Schnable Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pT713PAC; Site_1: EcoRI; Site_2: NotI; ds-cDNA molecules were generated as follows. First-strand cDNA was prepared from oligo-dT selected mRNA by priming
                                                                                              237 ACCACCACCACCATGGTCACCACGGCGGCCACGGCTTCGTGGTGCGCGAGACCAGGG
                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Iowa State University
G405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
Tel: 515-294-0975
                                                                ó
                                         Length 648;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fax: 515-42.

Email: schnable@lastate.c._
PCR PRimers
FORWARD: T7-1 (AA TAC GAC TCA CTA TAG)
BACKWARD: T7-1 (AA TAC GAC TCA CTA AG)
BACKWARD: T3 (ATT AAC CCT CAC TAA AG)
Seq primer: primer T7-1 (AA TAC GAC TCA TAG).
ES
Location/Qualifiers
Jource
//organism="rea mays"
//oultivar="B13"
//h xref="taxon:4577"
                                                              Indels
                                       DB 14;
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/lab_host="DH108"
                                   Score 261; DB
Pred. No. 0;
0; Mismatches
     100
   6
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                                  38.68;
  O
                                                                                                                                                                                                                                                                                                                           537 TCGTAATACTAA 548
                                              Best Local Similarity 99.7
Matches 311; Conservative
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 193
                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence.
BG840383
BG840383.2
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Zea mays
172
                                                                                                         233
                                   Query Match
BASE COUNT
ORIGIN .
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VERSION
KEYWORDS
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AUTHORS
TITLE
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Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta; Spermatophyta: Magnollophyta; Liliopsida: Poales; Poaceae; PACC clade; Pancooldeae: Andropogoneae; Zea.

1 (bases 1 to 546)

Expressed Squence Tags from B73 Maize Seedlings

L Unpublished (1997)

Contact: Schnable, PS

Schnable laboratory

Iowa State University

G405 Agronomy, Ames, IA 50011, USA

Tel: (515)-294-2299

Email: schnable@lastate.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA979839 546 bp mRNA linear EST 26-MAY-1998
MEST2-B7 TW1412.Seq ISUM2 2ea mays CDNA clone MEST2-B7 5', mRNA
                                                                                                                                                                                                                                                                               237 ACCACCACCACCACCATGGTCACCACGGCGCCACGGCTTCGTGGTGCGGCGAGACCAGGG 296
                                                                                                                                                                                                                                                                                                 297 ICGAGGAGGACAICAACACCIGCACCGGCGAGGICCACGAGCGCAGGGAAGGIICCICG 356
                                                                                                                                                                                                                                                                                                                                                              476
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BACKWARD: T7-YJ (5'-TAATACGACTCACTATAGGGC-3')
Plate: MST2 row: B column: 7
Seq primer: tw1412 (5'-GAAGATACCCCACCAACC-3').
Location/Qualifiers
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                                                                                                                                                                                                                    37.9%; Score 256; DB 1
99.7%; Pred. No. 0;
tive 0; Mismatches
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Gaps

142

138

258 322

262

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AW787315 436 bp mRNA linear EST 16-MAY-2000 945002E06.X2 945 - Mixed adult tissues from Walbot lab, same as 707 (SK) Zea mays cDNA, mRNA sequence.
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1 (bases 1 to 436)
Walbot,V.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          263 GGCGGCCACGGCTTCGTGGTGCGCGAGACCAGGGTCGAGGAGGACATCAACACCTGCACC
7300 NW 62nd Ave., P.O. Box 1004, Johnston, IA 50131-1004, USA Tel: 515 270 5934
Fax: 515 254 2619
Email: rudolf.jung@pioneer.com.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                        GCACCAATGGCTTACTACCAGGAGGTGGACTACTGCTCGGAGGAGGTGAGGTCGGTGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                 143 CCGGCCGGCTTCGGCCGCCGCCGCGGCGCGTCCAGCACGTCGTCAAGGAAGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maize ESTs from various cDNA libraries sequenced at Stanford
                                                                                                                                                  /organism="Zea mays"
/db_xref="taxon:4577"
/clone_lib="Pioneer AF-1 array"
/note="Vector: pSport1; Site_1: Sal1; Site_2: Not!"
150 c 133 g 53 t
                                                                                                                                                                                                                                                                                                                 Length 417
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; Pred. No. 0;
0; Mismatches
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Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 945002 row: E column: 06.
Location/Qualifiers
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Department of Biological Sciences
Stanford University
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/cultivar="W23"
/db_xref="taxon:4577"
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al Similarity 99.4%;
337; Conservative
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Unpublished (1999)
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AUTHORS
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AW787315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   237 ACCACCACCACCACCATGGTCACCACGGCGGCCACGGCTTCGTGGTGCGCGAGACCAGGG
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Trait and Technology Development, Food and Feed Research
Pioneer Hi-Bred International, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 255; DB 9; Length 546;
Pred. No. 0;
0; Mismatches 1; Indels
                                                                                                                                                                 /tissue_type="above ground tissues"
/dev_stage="Two-leaf-stage green seedling"
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/clone="MEST2-B7"
                                  1. .546
/organism="Zea mays"
/cultivar="B73"
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                                                                                                                                           /clone_lib="ISUM2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BM501439
BM501439.1 GI:18661517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 37.7%;
Best Local Similarity 99.7%;
Matches 305; Conservative
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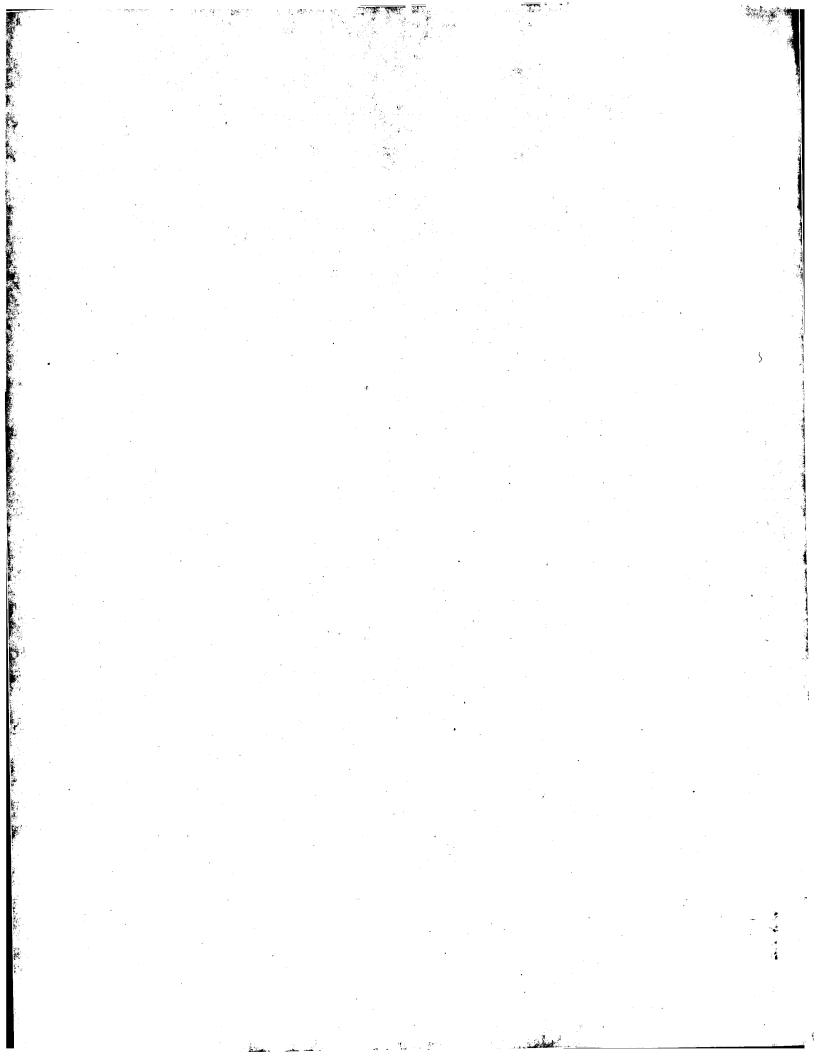
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/note="Organ: tassel, kernal, silk, husk, root, leaf; Vector: pGAD10; Site_1: EcoRI; cDNA library from fully differentiated malze tissues from an active Mutator plant. Tissue ratio is 4:2:1:1:1:1 (tassel, kernel, silk, husk, root, leaf). Unidirectionally cloned. New library number given to library 707 for additional sequencing."
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Search completed: June 16, 2003, 08:38:41 Job time: 1384.39 secs



Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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COMMand line parameters:

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-0-/cgn2_1/USPTO_spool_/USI0090035/runat_06062003_105504_10970/app_query.fasta_1.526
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-0-CALIGN=1 -END-1 -MATRIX-b100 -THR_MIN-0 -ALIGN=15 -MODE=LOCAL
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-0-OUTPMT-pto -NORM-ext -HERSIZE-500 -MINLEN-2000-1005004_10970 -NCPU-6 -ICPU-3
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-FGAPEXT-7 -YGAPOP=10 -YGAPEXT-0.5 -DELOP=6 -DELEXT-7
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0 , Xgapext (Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext
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A1964534 496013D01 A1964458 496010H04 A1855425 603016F02 AA979839 MEST2-B7. AY104409 Zea mays BQ619167 RNOSEQ4E0 BMS01439 417 bp mRNA linear EST 14-FEB-2002 PAC000000000593 Pioneer AF-l array Zea mays CDNA, mRNA sequence. MEST12-H1 15002E06 Description BQ619167 BQ619315 BQ619318 BQ619337 B AW745436 WBE593507 WBQ280894 WAW289056 7 BE599123 BQ280709 BE364814 AW924079 AW677917 AW746383 AW679713 AW925014 ALIGNMENTS AW680016 AW679969 AW289056 AW288875 BF729420 BG840383 AW745400 AW924079 AW677917 ü BM501439.1 GI:18661517 DB Match Length Zea mays. Zea mays Score 44233.5 4223.5 4444233.5 44223.5 4417.5 3683.5 3683.5 3683.5 3683.5 3683.5 3683.5 3683.5 3683.5 3683.5 3683.5 308 308 308 308 308 DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS RESULT 1 BM501439 LOCUS ş 000

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Zea.

1 (bases 1 to 417)

Hunter, B.G., Beatty, M., Singletary, G., Hamaker, B., Larkins, B.A. and Jung, R.

em\_gss\_other:\* em\_gss\_pro:\* em\_gss\_rod:\*

em\_gss\_mam:\* em\_gss\_mus:\* em\_gas\_fun:\*

em\_gss\_hum:\* em\_gss\_pln:\*

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gb\_est5

gb\_est3:

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EST: \*

Catabase :

em\_estpl:\* em\_estro:\*

gb\_est1:\*
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BE129897.1 GI:8577260
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 465)
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Trait and Technology Development, Food and Feed Research
Pioneer Hi-Bred International, Inc.
7300 NW 620d Ave., P.O. Box 1004, Johnston, IA 50131-1004, USA
Tel: 515 270 5934
Fax: 515 254 2619
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                                                                                                                                        /organism="Zea mays"
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/note="Vector: pSportl; Site_1: Sall; Site_2: NotI"
/ 150 c 133 g 53 t
   in
  Maize opaque endosperm mutations create extensive changes patterns of gene expression Unpublished (2002)
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Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
B55 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
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                                                                                                            Email: rudolf.jung@ploneer.com.
Location/Qualifiers
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/vector: pGAD10; Site_1: EcoRI; cDNA library from fully
differentiated malze tissues from an active Mutator plant.
Tissue ratio is 4:2:1:1:1:1 (tassel, kernel, silk, husk,
root, laaf): Unidirectionally cloned. New library number
given to library 707 for additional sequencing:"
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AW787732 IG::7844510
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
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Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
walbot@stanford.edu
945032 row: C column: 12.
Location/Qualifiers
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                                                                              /organism="Zea mays"
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tissues from Walbot lab (SK
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/note="Organ: tassel, kernel, silk, husk, root, leaf;
/note="Organ: tassel, kernel, silk, husk, root, leaf;
/note="Organ: tassel, kernel, silk, husk, root, leaf;
/differentiated malze tissues from an active Mutator
plant. Tissue railo is 4/2/1/1/1/1 (tassel, kernel, silk,
husk, root, leaf). Unidirectionally cloned."
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1 (bases 1 to 524)
Walbot, V.
Maize ESTs from various cDNA libraries sequenced at Stanford conversity.
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              Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 707049 row: E colunn: 04.
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/organism="Zea mays"
/cultivar="W23"
/db_xref="taxon:4577"
/clone_lib="707 - Mixed adult ti
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mays cDNA, mRNA sequence.
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                                                                                                       /db_xref="taxon.4577"
/clone_llb="945 - Mixed adult tissues from Walbot lab, same as 707 (St)"
/close_llb="1045 - Mixed adult tissues from Walbot lab, same as 707 (St)"
/clssue_type="tasse, kernal, silk, husk, root, leaf"
/lab_lost="blidg"
/note="Organ: tasse, kernal, silk, husk, root, leaf;
/vector: pGAD10; Site_1: EcoR1; cDNA library from fully differentiated maize tissues from an active Mutator plant.
Tissue ratio is 4:2:1:1:1:1 (tasse), kernel, silk, husk, root, leaf). Unidirectionally cloned. New library number given to library 707 for additional sequencing."
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tissues from Walbot lab (SK) Zea
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoldeae; Andropogoneae; Zea.
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Conservative:
Mismatches:
Indels:
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Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 945002 row: E column: 06.
Location/Qualifiers
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Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
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707049E04.x1 707 - Mixed adult t
mays cDNA, mRNA sequence.
AW331212 GI:6827569
                                                                                   /organism="Zea mays"/cultivar="W23"
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A1964458 496 - Stressed shoot cDNA library from Wang/Bohnert lab zea mays cDNA, mRNA sequence.
A1964458 A205451711
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC

Clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 481)

Walbot, V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .466 // Organism="Zea mays" // Organism="Zea mays" // Cultivar="B73" // Ab_xref="taxon:457" // Ab_xref="taxon:457" // Ab_xref="taxon:457" // Aponert lab" // Lissue_type="seedling" // Abs. stage="salt stress" // Ab_host="E.coli XL Gold" // Ab_host="E.coli XL Gold" // Ab_host="Coli XL Gold" // Ab_host=
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Department of Biological Sciences
Stanford University
Stanford University
Fal: 650 723 227
Fax: 650 725 8221
Fax: 650 496013 row: D column: 01.
Plate: 496013 row: D column: 01.
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Matches:
Conservative:
Mismatches:
Indels:
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Unpublic (1999)
Contact: Walbot V
Department of Biological Sciences.
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Wang/Bohnert
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/dev_stage="adult"
/lab_host="DHIOB"
/note="corpan: tassel, kernel, silk, husk, root, leaf;
/note="corpan: tassel, kernel, silk, husk, root, leaf;
/note="corpan: tassel, kernel, root, leaf;
/octor: pGADIO, Site_1: ECORI: cDNA library from fully
differentiated maize tissues from an active Mutator
plant. Tissue ratio is 4/2/1/1/1/1 (tassel, kernel, silk,
plant. Tissue ratio is 4/2/1/1/1/1 (tassel, kernel, silk,
plant. root, leaf). Unidirectionally cloned.
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/cultivar="w23"
/db_xref="taxon:4577"
/clone_lib="707 - Mixed adult tissues from Walbot lab
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                                              Stanford University
855 California Ave, Palo Alto, CA 94304, USA
855 California Ave,
Fax: 650 725 8221
Fax: 650 725 8221
Fax: 670 725 8221
Finall: Walbortestanford.edu
Plate: 707009 row: E column: 07.
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Matches:
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                     Department of Biological Sciences
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603016F02.x1 603 - stressed root cDNA library from Wang/Bohnert lab
AI855425
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                                                             Maize ESTs from various cDNA libraries sequenced at Stanford
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              CA 94304, USA
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Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
Stanford University
855 California Ave, Palo Alto, CA 94
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 496010 row: H column: 04.
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(organism="Zea mays"

(outiver="taxon:4577"

(db_xref="taxon:4577"

(clone_lib="603 - stressed root cDNA library from Wang/Bohnert lab"

(tissue_type="seedling"

(dev_stage="salt stress"

(lab_host="E. coli XL Gold"

/note="Organ: root; Vector: pBluescriptII SK(+) XR;

Seedling stressed root cDNA library from Wang/Bohnert lab"

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1 (bases 1 to 546)

2 Wen,T.J. Ashlock,D.A. and Schnable,P.S. Expressed Sequence Tags from B73 Maize Seedlings

L Unpublished (1997)

Contact: Schnable, PS

Schnable laboratory

Iowa State University

G405 Agronomy, Ames, IA 50011, USA

Tel: (515)-294-0975

Fax: (515)-294-2299

Email: schnable@lastate.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA979839 546 bp mRNA linear EST 26-MAY-1998
MEST2-B7.TW1412.Seq ISUM2 Zea mays cDNA clone MEST2-B7 5', mRNA
RA979839. GI:3157217
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Matches:
Conservative:
Mismatches:
Indels:
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 603016 row: F column: 02.
Location/Qualifiers
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499.50
98.948
98.948
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Qiu,F., Cui,F., Guo,L., Ashlock,D.A, Wen,T.J. and Schnable,P.S. Expressed Sequence Tags from B73 Maize Seedlings and Silks Unpublished (2001) on May 25, 2001 this sequence version replaced gi:14206705. Contact: Patrick S. Schnable Schnable Laboratory
                                                                                 Town State University

Iowa State University

G405 Agronomy, Iowa State University, Ames, IA 50011-1010, 18-15:15-294-0975

Fax: 515-294-2099

Email: schnable@iastate.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FORWARD: T7-1 (AA TAC GAC TCA CTA TAG)
BACKWARD: T3 (ATT AAC CCT CAC TAA AG)
Seg primer: primer T7-1 (AA TAC GAC TCA CTA TAG).
Location/Qualifiers
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Mismatches:
Indels:
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/tissue_type="Seedling and silk"
/lab_host="DH10B"
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Matches:
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/db_xref="taxon:4577"
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Best Local Similarity:
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AY104409
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                                                                                                                                                                                                  / tau_unsus_nair_wirk bild.
//note="Organ: green seedlings; Vector: pAD-GAL4; Site_1:
ECORI; Site_2: Xhoi; ds-CDNA molecules were generated as
ECORI; Site_2: Xhoi; ds-CDNA molecules were generated as
ECORI; Site_2: Xhoi; ds-CDNA was prepared from oligo-dr
selected mRNA by priming with an Xhoi oligo-dr primer. The
resulting DNA:RNA hybrid was treated with RNase H and used
as a template for DNA POII-catalyzed second strand
synthesis. After the addition of ECORI adaptors, the
ds-CDNAs were digested with Xhoi and size-selected. The
resulting molecules were directionally cloned into the
ECORI and Xhoi sites of the HybrizAP lambda vector
(Stratagene) and excised as pAD-GAL4 phagemids."

10 a 168 c 159 g 88 t lothers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEST12-H11.T7-1 ISUM4-TN Zea mays CDNA clone MEST12-H11 5', mRNA sequence.
BG840383.2 GI:14242676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              246 GGCCACGGCTTCGTGGTGCGCGGAGACCAGGGTCGAGGAGGAGGACTACACACCGGCCGCC 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 GlyHisGlyPheValValArgGluThrArgValGluGluAspIleAsnThrCysThrGly 79
                                                                                                                                                                   /tissue_type="above ground tissues"
/dev_stage="Two-leaf-stage green seedling"
/lab_host="XLI-MFR Blue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 GluValHisGluArgArgGluSerPheLeuAlaArgAlaAsn 93
                 PCR PRIMERS
FORMARD: tw1412 (5'-GAAGATACCCCACCAAACC-3')
BACKWARD: T7-YJ (5'-TAATACGACTCACTATAGGGC-3')
BACKWARD: T7-YJ (5'-GAAGATACCCCACCAAACC-3')
Seg primer: tw1412 (5'-GAAGATACCCCACCAAACC-3').
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Matches:
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/cultivar="B73"
                                                                              Location/Qualifiers
                                                                                                                                                        /clone_lib="ISUM2"
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1. .648
/organism="zea mays"
/db_xref="taxon.457"
/db_xref="taxon.457"
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/dev_stage="2 weeks old"
/note="vector: pBluescript SK+; Stressed 24 hours at 150
mM Nacl"
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RNOSEDGCO6_SK.abl Salt stressed Zea mays roots cDNA library Zea mays cDNA clone RNOSEDGCO6_SK.abl similar to No homology, mRNA sequence.
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Matches:
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                                                                                                                                                                                                Email: bohnertlab@life.uiuc.edu.
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                                                                                                                                                                                                                                                                                                                    183 g
                               GI:21621161
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          sequence.
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     HTC 25-MAY-2002
                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

1 (Jases I to 553)
Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
Overgo Probes
Unpublished (2002)

2 (Dasses I to 553)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BQ619167 648 bp mRNA linear EST 27-JUN-2002 RNOSEQ4E05_SK.abl Salt stressed Zea mays roots cDNA library Zea mays cDNA clone RNOSEQ4E05_SK.abl similar to No homology, mRNA
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                                                                                                                                                                                                        of
                                                                                                                                                                                                                                                                                /clone_lib="Maize Mapping Project/DuPont Cornsensus Library"
                                                                                                                                                                                      Direct Submission
Submitted (25-APR-2002) Maize Mapping Project, University Missouri, Columbia, MO 65211, USA
Location/Qualifiers
1. 553
/organism="Zee mays"
/db_xref="maizebB:637271"
/db_xref="taxon:4577"
/clone="PC0124784"
    linear
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Matches:
Conservative:
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    mRNA
Zea mays PCO124784 mRNA sequence. AY104409
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                                                                                                                                                                                                                                                                                                                                                                         162 g
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; PACC
clade; Panicoldeae; Andropogoneae; 2ea.
                                                                                                                                                                               /clone="RNOSESOGG6_SK.abl"
/clone_lib="Salt stressed Zea mays roots cDNA library"
/tissue_type="Roots"
/dev.stage="2 weeks old"
/note="Vector: pBluescript SK+; Stressed 24 hours at 150
                                                                                                                                                                                                                                                                                                                                                                                    21 GlyPheGlyArgHisGlyGlyGlyValGlnGlnHisValValLysGluLysPheGluGlu
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                                  Matches:
Conservative:
Mismatches:
Indels:
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Wang,H. and Bohnert,H.J.
Genomics of plant stress tolerance
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BQ619337 648 bp mRNA linear EST 27-JUN-2002 RNOSEQ6E12_SK.abl Salt stressed Zea mays roots cDNA library Zea mays cDNA clone RNOSEQ6E12_SK.abl similar to No homology, mRNA
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1 (bases 1 to 648)

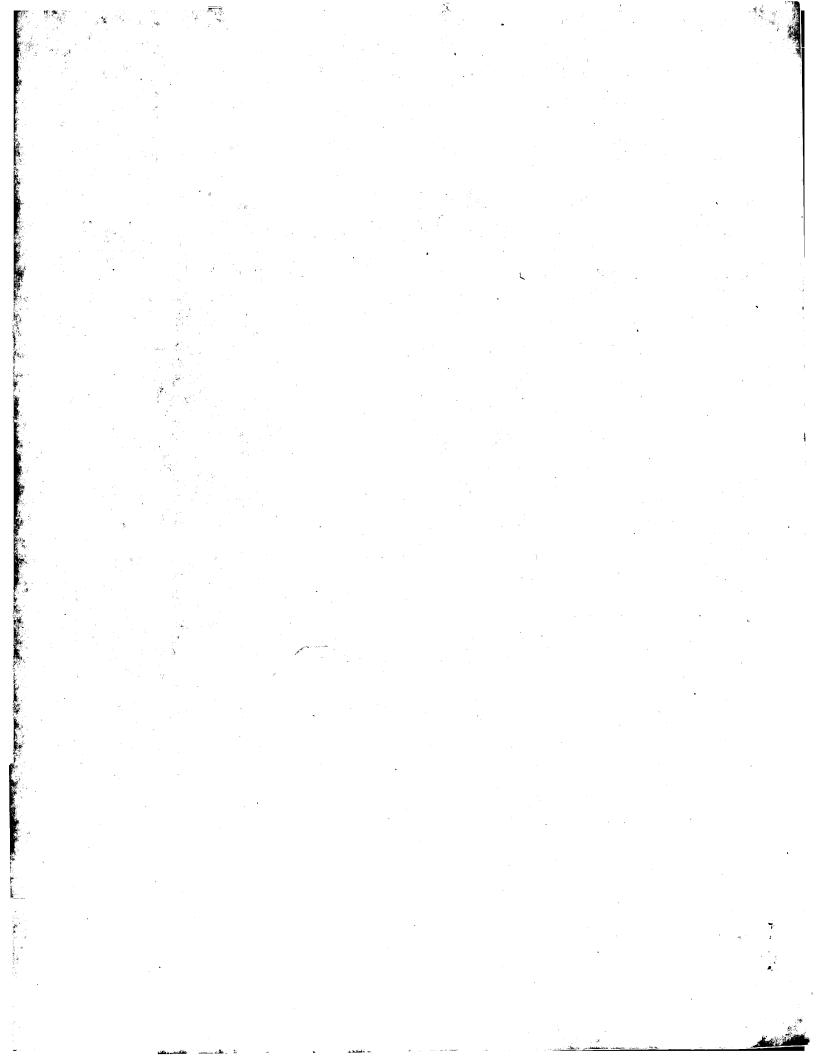
Wang, H. and Bohnert, H.)

Genomics of plant stress tolerance
Unpublished (2002)

Contact: Mark Fredicksen
Department of Plant Biology
University of Illinois

1201 W. Gregory Dr., Urbana, IL 61801, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mays roots cDNA library"
                                                                                                                                                                                                Stressed 24 hours
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93
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Unpublished (2002)
Contact: Mark Fredricksen
Department of Plant Biology
University of Illinois
1201 W. Gregory Dr., Urbana, IL 61801, USA
Tel: 217265573
Email: bohnertlab@life.uiuc.edu.
                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                /organism="Lea mays"
/db_xref="taxon:4577"
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Email: bohnertlab@life.uiuc.edu.
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mM NaCl"
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Copyright (c) 1993 - 2003 Compugen Ltd.
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## ALIGNMENTS

AW924579 W21677 BQ283209

RESULT 1 AT104409 LOCUS DEFINITION ACCESSION VERSION VERSION KEYNORS SOURCE ORGANISM TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL REFERENCE SOURCE	AY104409  Zea mays AY104409  Zea mays AY104409  AY104409  AY104409  AY104409.1 GI:21207487  HTC. Zea mays  Arthurioldese; Andropogoneae; Zea.  1 (bases 1 to 553)  Zea C.  Zea Lo 553)  Zea C.  Zea Lo 553)  Zea Lo 553  Zea Lo
	RESULT 1 AT104409 LOCUS LOCUS DEFINITION ACCESSION VERYORS SOURCE ORGANISM TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL FEATURES SOURCE

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

em\_gss\_fun: \*
em\_gss\_mam: \*
em\_gss\_mus: \*
em\_gss\_other: \*
em\_gss\_pro: \*

em\_gss\_pln:\*

gb\_est2:\*
gb\_ntc:\*
gb\_est3:\*
gb\_est4:\*
gb\_est5:\*
em\_est5i:\*
em\_est6m:\*
gp\_gss:\*
em\_gss\_lnu:\*
em\_gss\_lnu:\*

SUMMARIES

<u>B</u>B

Length

Ouery Match

Score

Result No. AY104409 Zea mays BE025302 945028B09 AA979839 MEST2-B7. AW288876 707009E07 AW331212 707049E04 BO619167 RNOSEQ4E0

AX104409 BE025302 AA979839 AW288876 AW331212 BQ619167

100011

90.8 90.2 88.8 87.2

521.2 518 509.6 507.2 500.8

Description

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AA979839 546 bp mRNA linear EST 26-MAY-1998
MEST2-B7.TW1412.Seq ISUM2 Zea mays CDNA clone MEST2-B7 5', mRNA
                                                                                                                                                                                                                             /note="Organ: tassel, kernal, silk, husk, root, leaf; vector: pGAD10; Site_1: ECORI; cDNA library from fully differentlated maize tissues from an active Mutator plant. Tissue ratio is 4:2:1:1:1:1 (tassel, kernel, silk, husk, root, leaf). Unidirectionally cloned. New library number given to library 707 for additional sequencing."
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/clone_lib="945 - Mixed adult tissues from Walbot lab,
same as 707 (SK)"
                                                                                                                                                                                           root, leaf"
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      Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 9,
Tel: 650 723 2227
Fax: 650 725 8221
                                                                                    Email: walbot@stanford.edu
Plate: 945028 row: B column:
Location/Qualifiers
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                             "Anote-"this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Malze Mapping Project" 90 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCGTCGGCACCAATGGCTTACTACCAGGAGGTGGACTACTGCTCGGAGGAGGTGAGGTCG
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                                                                                                                                                                                           Gaps
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/clone_lib="Maize Mapping Project/DuPont Cornsensus
Library"
                                                                                                                                          Score 521.2; DB 11; Length 553;
Pred. No. 1.7e-68;
0; Mismatches 8; Indels 3;
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945028B09.Yl 945 - Mixed
(SK) Zea mays cDNA, mRNA
BE025302
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                                                                                                                                               90.8%;
11 Similarity 98.0%;
539; Conservative
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1 (bases 1 to 524)

Walbot, V.
Malze ESTs from various cDNA libraries sequenced at Stanford University
University
University
University
Department of Biological Sciences
Stanford University
Stanford University
Biological Sciences
Stanford University
Fal: 650 723 2227
Fal: 650 723 2227
Fal: 650 723 2227
Fax: 650 728 8221
Email: walbottestanford.edu
Plate: 707009 row: E column: 07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA linear EST 16-JAN-2000 tissues from Walbot lab (SK) 2ea
                                                                                                                             /note="Organ: tassel, kernel, silk, husk, root, leaf;
Vector: pGAD10; Site_1: EcoRI: cDNA library from fully
differentiated maize tissues from an active Mutator
plant. Tissue ratio is 4/2/1/1/1/1 (tassel, kernel, silk,
husk, root, leaf). Unidirectionally cloned.

170 c 157 g 89 t 1 others
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  /db_xref="taxon:4577"
/clone_lib="707 - Mixed adult tissues from Walbot lab
/
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/dev_stage="adult"
/lab_host="DH10B"
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Best Local Similarity 99.0%; Pred. No. 2.1e-66;
Matches 520; Conservative 0; Mismatches 4; Indels 1;
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/organism-"Zea mays"
/cultivar-"W23"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon.4577"
/clone="MEGT2-87"
/clone=lb=1250M2"
/tlssue_lrb="150M2"
/tlssue_type="above ground tissues"
/tlssue_type="above ground tissues"
/dev_stage="Two-leaf-stage green seedling"
/lab_lost="All-NRR Blue"
/note="Organ: green seedlings; Vector: pAD-GAL4; Site_1:
ECORI; Site_2: Xhoi; ds-cDNA molecules were generated as follows. First-strand cDNA was prepared from oligo-dr selected mRNA by priming with an XhoI oligo-dr primer. The resulting DNA:RNA hybrid was treated with RNAse H and used as a template for DNA POII-cetalyzed second strand synthesis. After the addition of EcoRI adaptors, the resulting molecules were directionally cloned into the ECORI and XhoI sites of the Hybrizap lambda vector
(Stratagene) and excised as RD GAL4 phagemids."
                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Agenmatophyta; Spermatophyta; Clade; Panicoideae; Pan
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                                                                                                                                                                                                                        Wen, T.J., Ashlock, D.A. and Schnable, P.S.
Expressed Sequence Tags from B73 Maize Seedlings
Unpublished (1997)
Contact: Schnable, PS
Schnable laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plate: MEST2 row: B column: 7
Seq primer: tw1412 (5'-GaaGATACCCCACCAAACC-3').
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                              IOWA State University
G405 Agronomy, Ames, IA 50011, USA
Tel: (515)-294-0975
Fax: (515)-294-2299
Email: schnable@lastate.edu
PCR PRImers
FORWARD: T7-YJ (5'-GAAGATACCCCACCAAACC-3')
BACKWARD: T7-YJ (5'-TAATACGACTCACTATAGGGC-3')
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/organism="Zea mays"
/cultivar="B73"
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                                                523;
Unidirectionally cloned."
                                                 Length
                                          Score 500.8; DB 10; Leuser.
Pred. No. 1.9e-65;
'''-matches 7; Indels
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Wang, H. and Bohnert, H.J.
Genomics of plant stress tolerance
Unpublished (2002)
Contact: Mark Fredricksen
Contact: Mark Fredricksen
Department of Plant Biology
University of Illinois
                                                                         0; Mismatches
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Tel: 2172655473
Email: bohnertlabelife.uluc.edu.
Location/Qualifiers
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/db_xref="taxon:4577"
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158 c 149.g
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tissues from Walbot lab (SK) Zea
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/lab_host="DH10B"
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/note="Organ: tassel, kernel, silk, husk, root, leaf;
determinated maize tissues from an active Mutator
plant. Tissue ratio is 4/2/1/1/1/1 (tassel, kernel, silk,
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                         GGTGGCCCCGGCCGGCTTCGGCCGCCGCGGCGGCGTCCAGCAGCACGTCGTCAAGGA
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         AGCGTCGGCACCAATGGCTTACTACCAGGAGGTGGACTACTGCTCGGAGGAGGTGAGGTC
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Department of Biological Sciences
Stanford University
Stanfornia Ave, Palo Alto, CA 94304, USA
Tel: 650 723 227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 707049 row: E column: 04.
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/cultivar="W23"
/db_xref="taxon:4577"
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707049E04.xl 707 - Mixed adult t
mays cDNA, mRNA sequence.
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Department of Plant Biology
University of Illinois
University of Illinois
Tell W. Gregory Dr., Urbana, IL.
Tell: 2172655473
Email: bohnertlab@life.uiuc.edu.
Location/Qualifiers
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            mays roots cDNA library"
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ilarity 97.6%; Pred. No. 1.8e-65;
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/tlssue_type="Roots"
/dev_stage="2 weeks old"
/dev_stage="2 weeks old"
/note="Vector: pBluescript SK+;
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Wang, H. and Bohnert, H.J.
Genomics of plant stress tolerance
Unpublished (2002)
Contact: Mark Fredricksen
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1. .648
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2E 1 (bases 1 to 648)

RS Wang, H. and Bohnert, H.J.

Genomics of plant stress tolerance

AL Unpublished (2002)

Contact: Mark Fredricksen

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University of Illinois

1201 W. Gregory Dr., Urbana, IL 61801, USA

Tel: 2172655473

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Location-Trace Trace mays roots cDNA library"

//clone="RNOSEQ6D01_SK.abl"

//clone="RNOSEQ6D01_SK.abl"

//dev_stage="Rooter: pBluescript SK+; Stressed 24 hours at 150

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Pred. No. 1.8e-65;
0; Mismatches 9;
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Wang, H. and Bohnert, H.J.
Genomics of plant stress tolerance
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                 Contact: Mark Fredricksen
Department of Plant Biology
University of Illinois
1201 W. Gregory Dr., Urbana, IL 61
Tel: 2172655473
Email: bohnertlab@life.uluc.edu.
    648 bp
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                                                                                                                 GI:21621331
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC

Clade; Panicoideae; Andropogoneae; Zea.

S Wang, H. and Bohnert, H.J.

Genomics of plant stress tolerance

Unpublished (2002)

AL Unpublished (2002)

Robertment of Plant Bailogy

University of Illinois

1201 W. Gregory Dr., Urbana, IL 61801, USA

Tel: 2172655473

Fel: 2172655473

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                           BQ619390 648 bp mRNA linear EST 27-JUN-2002 RNOSEQ7B09_SK.abl Salt stressed Zea mays roots cDNA library Zea mays cDNA clone RNOSEQ7B09_SK.abl similar to No homology, mRNA
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/db_xref="taxon:4577"
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/tissue_type="Roots"
/dev_stage="2 weeks old"
/note="Vector: pBluescript SK+; Stressed 24 hours at 150
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Pred. No. 1.8e-65;
0; Mismatches 9; Indels 4;
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Best Local Similarity 97.6%;
Matches 530; Conservative
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC lade; Panicoldeae; Andropogoneae; Zea.

( Dases 1 to 648)
Wang,H. and Bohnert,H.J.
Wang,H. and Bohnert,H.J.
Confact: Mark Fredricksen
Unpublished (2002)
Contact: Mark Fredricksen
University of Illinois
University of Illinois
1201 W. Gregory Dr., Urbana, IL 61801, USA
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Location/Qualifiers
1. .648
/organism="Zeu mays"
/db_xref="taxon:4577"
/clone="RNOSEQ7B02_SK.abl"
/clone="TROSEQ7B02_SK.abl"
/clone="TROSEQ7B02_SK.abl
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RNOSEQ7B02_SK.abl Salt stressed Zea mays roots cDNA library Zea
mays cDNA clone RNOSEQ7B02_SK.abl similar to No homology, mRNA
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BG840383
BG840383.2 GI:14242676
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1 (basea: Ito 550)
1 (basea: Ito 550)
2 (u.F., Cul.F., Guo.L., Ashlock,D.A, Wen,T.J. and Schnable,P.S. Expressed Sequence Tags from B73 Maize Seedlings and Silks Unpublished (2001)
2 (On May 25, 2001 this sequence version replaced gi:14206705.
                                                                                                                                                                   391
                                                              380
                                                                                   451
                                                                                             331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G405 Agronomy. Iowa State University, Ames, IA 50011-1010, USA Tel: 515-294-0975
Fax: 515-294-2299
Email: schnable@iastate.edu
CGAGGTCCACGAGGCAGGGAGGCTTCCTCGCCAGGGCTAACTGAGCCGCCGGCGGCC
                                                     GITCAGGGTCATCGIACTIGGCIATCGIACGIGCACGCACTCAGCTCCTGIACGAATTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  primer: primer T7-1 (AA TAC GAC TCA CTA TAG).
Location/Qualifiers
1. 550
/organism="Zea mays"
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/clone="MEGT12-H11"
/clone=lb="ISGN4-TN"
/tissue_type="Seedling and silk"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FORWARD: T7-1 (AA TAC GAC TCA CTA TAG)
BACKWARD: T3 (ATT AAC CCT CAC TAA AG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cultivar="B73"
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G405 Agronomy, Iowa St
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AI855425
603016F02.x1 603 - stressed root cDNA library from Wang/Bohnert lab
resulting molecules were directionally cloned into the EcoRI and NotI sites of the pT713PAC vector. The library then went through one round of normalization to CoT value of 5 based on the methods of Marcelo Bento Soares (Genome Research 6: 791-806, 1996)."

174 c 159 g 92 t 1 others
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                                                                                                                                                           Gaps
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                                                                                                                            Length 550;
                                                                                                                                                           Indels
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                                                                                                                               DB 12;
                                                                                                                              Score 494.6; DB 12;
pred. No. 1.5e-64;
0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zea mays cDNA, mRNA sequence.
AI855425
AI855425.1 GI:5499558
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855 California Ave, P
Tel: 650 723 2227
Fax: 650 725 8221
                                                                                                                               86.2%;
llarity 97.6%;
Conservative
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524; Conserv
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Zea mays
                                                                                      Q
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Stanford

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/note="Organ: tassel, kernal, silk, husk, root, leaf; vector: p6AD10; Site_1: EcoR: cona active Mutator plant differentiated maize tissues from an active Mutator plant. Tissue ratio is 4:2:1:1:1:1 (tassel, kernel, silk, husk, root, leaf). Unidirectionally cloned. New library number given to library 707 for additional sequencing."
                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 GCGCTGCGCACAGACACCAAGCGTCGGCACCAATGGCTTACTACCAGGAGGTGGACTA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. :500

/organism="zea mays"
/organism="zea mays"
/db.xref="xea"
/clone_lib="945 - Mixed adult tissues from Walbot lab,
same as 707 (SK)"
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/dev_stage="fully-grown"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 CTGCTCGGAGGAGGTGAGGTCGGTGGCCCCGGCCTTCGGCCGCCGCCACGGCGGCGGCGT
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                                                                                                                                                                                                                                                                                                                                                                                                 Score 485.8; DB 10; Length 500;
Pred. No. 3.2e-63;
0; Mismatches 2; Indels 0;
            sedneuced
                                                      Department of Biological Sciences Stanford University Palo Alto, CA 94304, USA Tel: 650 723 2227
Fax: 650 725 8221
Email: walbotrestanford.edu
Plate: 945002 row: E column: 06.
          cDNA libraries
          ESTs from various
                                                                                                                                                                                                                                                                                                                                                                                                 84.6%;
99.6%;
        Maize ESTs from va
University
Unpublished (1999)
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Best Local Similarity 99.69
Matches 487; Conservative
                                              Contact: Walbot V
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                                    / ..539
/ Organism="Zea mays"
/ Coultivar="B37"
/ Ab_xref="taxon:4577"
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/ tab_host="E. coli XL Gold"
/ note="Organ: root; Vector: pBluescriptII SK(+) XR;
Seedling stressed root cDNA library from Wang/Bohnert lab"
157 c 172 g 119 t library from Wang/Bohnert lab"
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Zea mays.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 500)
Walbot, V.
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                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                          Length 539;
                                                                                                                                                                                                                   Match 86.1%; Score 494.4; DB 9; Local Similarity 97.2%; Pred. No. 1.6e-64; es 525; Conservative 0; Mismatches 11;
          603016 row: F column: 02.
Location/Qualifiers
1. 539
 walbot@stanford.edu
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Email:
Plate:
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Best Local S
Matches 525
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ORIGIN
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KEYWORDS
SOURCE
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AUTHORS
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Gaps

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301 240 361 300 421 360 420

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/note-"Organ: tassel, kernal, silk, husk, root, leaf; vector: pGAD10; Site_1: ECORI; cDNA library from fully differentiated maize tissues from an active Mutator plant. Tissue ratio is 4:2:1:1:1:1 (tassel, kernel, silk, husk, root, leaf). Unidirectionally cloned. New library number given to library 707 for additional sequencing."
AW787314 496 bp mRNA linear EST 16-MAY-2000 945002E06.X1 945 - Mixed adult tissues from Walbot lab, same as 707 (SK) Zea mays cDNA, mRNA sequence.
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Walbot,V.
Walbot,V.
Walse Erss from various cDNA libraries sequenced at Stanford University
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .496
/organism="zea mays"
/oultivar="W23"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="tassel, kernal, silk, husk, root, leaf"
/dev_stage="fully-grown"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                                                                                                                Contact: Walbot V
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 728 821
Email: walbot@stanford.edu
Plate: 945002 row: E column: 06.
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Pred. No. 3.2e-60;
0; Mismatches 4.
                                                                         AW787314.1 GI:7844111
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99.0%;
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                                                                                                             Zea mays.
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Best Local S:
Matches 479;
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173
        16.1
       83
       17
                                                                          June 6, 2003, 12:47:53 ; Search time 50 Seconds (without alignments) 383.248 Million cell updates/sec
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510
1 MAYYQEVDYCSEEVRSVAPA.....INTCTGEVHERRESFLARAN 93
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                               671580 seqs, 206047115 residues
                                                 OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
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sp_invertebrate:*
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Q880bl oryza sativ O9sm40 sporobolus Q880b2 oryza sativ Q92w63 arabidopsis Q94w63 arabidopsis Q95w463 arabidopsis Q9543 neurospora Q880b4 oryza sativ Q9usy0 caenorhabdi Q94l7 arabidopsis Q94z3 arabidopsis Q94q7 arabidopsis Q94x3 arabidopsis Q94wm5 drosophila Q90ww0 petromyzon Q9nes7 caenorhabdi Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Description SUMMARIES Q8S0B4 Q9UAXO Q9Y2L9 Q9Y4Q7 Q9FZ33 Q9W3D2 Q9WWM5 Q9OWVO Query Match Length DB Score 92.5 92.5 92.5 86.5 86.5 86.5

Result No.

RESULT 2 Q9SM40

82.5 82.5

091f59 arabidopsis 020691 caenorhabdi 020699 caenorhabdi 04248 medicago sa 09nc84 strongyloca 09f244 arabidopsis 09f244 arabidopsis 09f244 arabidopsis 09f24 arabidopsis 09f26 drosophila 09uti drosophila	•	ď	lpdate)	Embryophyta; Tracheophyta; ; Poales; Poaceae;	chromosome 1, PAC BJ databases.	F61E CRC64;	10; Length 229; -23; Indels 4; Gaps 2;	(EKFEEVDTVSRAGANHHHHGHHGG 60       :  :       :	7
16.1 173 10 09LF59 15.9 86 5 020691 15.9 191 10 04246 15.9 191 10 04246 15.8 347 5 09VXC84 15.8 347 5 09VXC84 15.8 36 10 09FH24 15.7 1273 4 060316 15.5 612 10 09FH24 15.3 156 10 094189 15.3 156 10 08VXVR 15.3 156 10 09VXVR 15.3 156 10 09VXVR 15.3 156 5 09VXVR 15.2 537 5 09VXVR 15.2 549 5 09VXVR 15.2 1693 5 09VXVR 15.1 509 5 09VXR 15.1 509 5 09V	ALIGNMENTS	PRELIMINARY; PRT; 229 AA	(TrEMBLrel. 21, Created) (TrEMBLrel. 21, Last sequence update) (TrEMBLrel. 21, Last annotation updat	Oryza sativa (japonica cultivar-group). Eukaryota, Viridiplantae, Streptophyta; Emb Spermatophyta; Magnollophyta; Liliopsida; P Ehrhartoldeae; Oryzeae; Oryza.	PPONBARE; tsumcto T., Yamamoto K.; nipponbare(GA3) genomic DNA, ch. 2.;	9 AA; 25296 MW; D6ED4AA65FFEF61E	53.7%; Score 274; DB 10; ilarity 58.1%; Pred. No. 4.96-23; Conservative 14; Mismatches 21	AYYQEVDYCSEEVRSVAP-AGFGRHGGGVQOHVVKEKFEEVDTVSRAGANHHHHGHHGG   :	HGEVVRETRVEEDINTCTGEVHERRESFLARAN 9 :    :
177 82 177 5 23 80 17 18 81 18 81 22 24 80 15 25 80 15 25 80 15 25 80 15 25 80 15 25 80 15 25 80 15 25 80 15 25 80 15 25 80 15 25 80 15 25 80 15 25 80 15 25 80 15 25 80 15 25 80 15 25 80 15 25 80 15 25 80 15 25 80 15 25 80 15 25 80 15 25 80 15 25 80 15 25 80 15 25 80 15 25 80 15 25 80 15 25 80 15 25 80 15 25 80 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20 15 20		RESULT 1 2880B1 ID Q880B1 AC 0880B1.	01-JUN-2002 01-JUN-2002 01-JUN-2002 P0470A12.5 P	Oryza sativa Eukaryota; V Spermatophyt. Ehrhartoidea: NCBI_TaxID=3:	SEQUENCE FROM N.A. STRAIN-CV. NIPPONBARE; Sasaki T., Matsumoto T., "Oryza sativa nipponbare clone:P0470A12."; SUBMILLEA (MAR. 2011) to FWRI.	3	Query Match Best Local Similarity Matches 54; Conser	2 AYYQ   : 140 AQEK	61 HGFV : 197 DYLM
		RES Q8S ID	DT DT SE	80008	RP SER RA SER RT CO RT CD RE SM	os '	O E E	ර් සි	Oy Db

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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLRel. 21, Last an
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SEQUENCE FROM N.A.
Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Hayashizaki Y.,
Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
Ishida J., Jang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
Ishida J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
Rawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
Satou M., Seki M., Southwick A., Tang C.C., Torlumi M., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
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          Ar4936900/C7Al0.460.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 196;
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33.8%; Pred. No. 0.013;
...matches 24; Indels
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; Z99707; CAB16766.1;
EMBL; AL161590; CAB80356.1;
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
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"Arabidopsis CDNA CLONES.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AXO57683; AAL15314.1;
InterPro; IPR001471; TF_ERF.
ProDom: PF00147; AP2-domain; 1.
ProDom: P001423; TF_AP2; 1.
SEQUENCE 196 AA: Z1392 MW; E423D5570745C9CD CRC64;
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Interpro; IPR001471; TF_ERF.
Pfam; PF00847; AP2-domain; 1.
PRINTS; PR00367; ETHRSPELENT.
PRODOM; PD001423; TF_AP2; 1.
SMART; SM00380; AP2; 1.
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159 INDDLMECSSK 169
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Best Local S
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                                                                                                                                            Putative glycine-rich protein.
Sporobolus stapfianus (Ressurection grass).
Bukaryota; Viridiplantae; Srreptophyta; Embryophyta; Tracheophyta; Sperimatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Chloridoideae; Eragrostideae; Sporobolus.
NCBI_TaxID=56623;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoldeae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Neale A.D., Blomstedt C.K., Bronson P., Le T.N., Guthridge K.,

Byans J., Gaff D.F., Hamill J.D.;

"The isolation of lowly-transcribed genes which are induced during dessication of the resurrection grass Sporobolus stapfianus.";

Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, AJ242802; CAB61838.1;
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"Orgas astiva hipponbare(GA3) genomic DNA, chromosome 1, PAC clone:P0470A12.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AP003436; BAB90279.1; --
SEQUENCE 102 AA; 11214 MW; 6FF1266B1CDE7768 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27.6%; Score 141; DB 10; Length 102;
45.8%; Pred. No. 2e-08;
ive 8; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        8802; CAB61838.1; -.
95 AA; 10668 MW; D756DCE2B68DD85B CRC64;
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0932A6, 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
                                                                                  OL-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 177; DB 10;
Pred. No. 1.5e-12;
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45; Conservative
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Related to multifunctional cyclin-dependent kinase PHO85 B24H17.10.
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72.2%;
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InterPro; IPR004129; GDPD.
InterPro; IPR004331; SPX.
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Matches 13; Conservative
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Pfam; PF03009; GDPD; 1.
Pfam; PF03105; SPX; 1.
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                                Neurospora crassa.
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                                                                        WEDLINE-97338147; PubMed-9192694;

X MEDLINE-97338147; PubMed-9192694;

A Okamuro J. K., Caster B., Villarroel R., van Montagu M., Jofuku K.D.;

RT The AP2 domain of APETALA2 defines a large new family of DNA binding

RT Proceins in Arabidopsis.;

R Proc. Natl. Acad. Sci. U.S.A. 94:7076-7081(1997).

BR MEBL; A7002598; CAA05630.1; -

BR MESP; 080337; 2GCC.

DR MESP; 080337; 2GCC.

DR PRESP: PRO01471; TF_ERF.

DR PRIWES; PR00367; ETHRSPELEMNT.

DR PRIWES; PR00367; ETHRSPELEMNT.

DR PRODOM; PD001423; TF_AP2; 1.
                                                           21 GFGRHGGG-VQQHVVKEKFEE----VDTVSRAGA---NHHHHGH-HGGHGFVVRET--R 69
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                     18.1%; Score 92.5; DB 10; Length 196; 33.8%; Pred. No. 0.013; Live 12; Mismatches 24; Indels 11; Gaps
                                                                                                                                                                                               01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
11NY-11ke protein (Fragment).
Arabidopsis thalian (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
NCBI_TaxID=3702;
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 21362 MW; 0023D5571345C6A0 CRC64;
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Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases
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259 AA; 28615 MW; 0464949DB6C619DB CRC64;
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                                          Conservative
                                                                                                                   159 INDDLMECSSK 169
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INDDLMECSSK 232
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  196 AA;
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les 24; Conserv
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                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                  STRAIN-COLUMBIA;
 SECUENCE
                    Query Match
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SEQUENCE
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Q9P543;
                                        datches
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024643
ID 0246
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ID 099
AC 099
DT 011
DT 011
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                                                                                                                                     ξ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                     [1]
SEQUENCE FROM N.A.
SCHUILE U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland I
Nyakatura G., Mewes H.W., Mannhaupt G.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
Eukaryota; Fung1; Ascomycota; Pez1zomycot1na; Sordarlomycetes;
Sordarialise; Sordarlaceae; Neurospora.
NCBI_TaxID=5141;
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STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
Toryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC clone:P0470A12."
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AP003436; BAB90277.1;
SEQUENCE 408 AA; 43466 MW; F7E0297877F6D69C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 17.0%; Score 86.5; DB 10; Length 408; Best Local Similarity 26.9%; Pred. No. 0.15; Matches 25; Conservative 10; Mismatches 15; Indels 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 89; DB 3; Length 1245; Pred. No. 0.29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANK repeat; Cyclin; Kīnasē; Repeat.
SEQUENCE 1245 AA; 137798 MW; 16BD0F6A04596A9F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                             German Neurospora genome project;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AL356815; CAB92623.1;
HSSP; P42773; lIHB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
P0470Al2.2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMATT, SM00248; ANK, 3.
PROSITE; PS50088; ANK_REPEAT; 3.
PROSITE; PS50297; ANK_REP_REGION; 1.
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Ecker J.R.
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STRAINBERISTOL NO.

WEDLINE-94150718; PubMed-7906398;

Wallson R., Anscough R., Anderson K., Baynes C., Berks M.,

Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,

Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,

Jones M., Green P., Hawkins T., Hillier L., Jet M., Johnston L.,

Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,

Lighthing J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,

Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,

Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,

Thierry Mieg J., Thomas K., Vaudin M., Vaughan R., Waterston R.,

Watson A., Weinstock L., Willkinson-Sproat J., Wohldman P.;

Watson A., Wolls on nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----GVQQHVVKEKFEEVDTVSRAGANHHHHG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25; Gaps
                                                                                                           Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases. EMBL, AF125964; AAD14753.1; -SEQUENCE 4711 AA: 50885 MW. PRP270E607641000
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
Pauley A., Scheet P., Harper M.;
"The sequence of C. elegans cosmid W03G1.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NAR-2002 (TrEMBLrel. 20, Last annotation update)
MIRATOLE protein (Fragment).
                                                                       01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2001 (TrEMBLrel. 17, Last annotation update)
W03G1.5 protein.
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                                                471 AA
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                                                 PRT;
                                                  PRELIMINARY; .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 RSVAPAGFGRHGG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                         Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             427 PPHHGHHFF 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57 -- HHGGHGF 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN=BRISTOL N2;
                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KIAA1016
                                                                                                                                                                                                                                                                                                                                                 elegans."
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                                                               Q9UAY0;
                                                   O9UAYO
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Q9Y2L9
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Matches
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MEDLINE-9944005; FUDRECI-LUCAIDAZ;

A NAGASE T., IShikawa K., Suyama M., Alkuno R., Hirosawa M.,

A Miyajima N., Tanaka A., Suyama N., Ohara O.;

A Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;

A Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;

RT The complete sequences of unidentified human genes. XIII.

RT The complete sequences of unidentified human genes. XIII.

RT The complete sequences of unidentified human genes. XIII.

RT The complete sequences of unidentified human genes. XIII.

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RT The Complete sequences of unidentified human genes. XIII.

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REPORT OF PROJATIS CALPONIN-LIKE.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

Cheuk R., Chen H., Kim C.J., Koesema B., Meyers M.C., Banh J.,

Cheuk R., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,

Bowser L., Carninci P.X., Jones T., Kaniya A., Karlin-Nemann G.

Ishida J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,

Rawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,

Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,

Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,

Tamamira Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 DYCSEEVRSVAPAGFGRHGGGVQOHVVKEKFEEVDTVSRAGANHHHHHHH----HGGH 61
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At1954990/F14C21_5.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TAXID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16.9%; Score 86; DB 4; Length 793; 32.8%; Pred. No. 0.37; .tive 7; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16.5%; Score 84; DB 10; Length 44 36.8%; Pred. No. 0.31; tive 10; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Arabidopsis cDNA clones.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF42460; AALI1602.1; -
SEQUENCE 441 AA, 48816 MW; 520163FE0ABDE447 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0BE99CC48C3BB37C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             441 AA
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PROSITE; PS00589; PTS_HPR_SER; UNKNOWN_1.
MEDLINE=99246063; PubMed=10231032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_TER 1 1
SEQUENCE 793 AA; 87801 MW;
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Best Local Similarity 36.8%;
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 16.9
Best Local Similarity 32.8
Matches 22; Conservative
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RC STRAIN-CV COLUMBIA;

RX MEDLINE-21016719; PubMed-11130712;

RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar R.,

RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fulji C.Y.,

RA Gill J.E., Goldsmith A.D., Hans B., Hansen N.F., Hughes B., Huizar L.,

RA Hunter J.L., Jonkins J., Johnson-Hopson C., Khan S., Khaykin E.,

RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

RA Militscher J., Mirenda M., Nguyen M., Nierman W.C., Osborne B.I.,

RA Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Sakano H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

Nuterback T., Van Aken S., Vaysberg M., Vysotskala V.S., Walker M.,

"Sequence and analysis of chromosome I of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wanda K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
A Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
A Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
A Tang C., Toriumi M., Wh H.C., Yamamura Y., Yu G., Bowser L.,
A Raniya A., Karlin Neumann G., Kawai J., Kim C., Lam B., Lin J.,
A Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
A Sakurai T., Satou M., Saki M., Shinn P., Southwick A., Shinozaki K.,
R. Pull Length cDNA of gene Arig$4990 (GI:15221965).";
B. Lubmitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; ACO64940; AAGO0878.1;
B. EMBL; ACO64940; AAGO0878.1;
B. EMBL; AVO7434; AAG57030.1;
377 DYISEFV-SLLPKSIRR----VAEEPIPEEVQKVLEEAKAGDDHDHHGHGHAHAGY 428
                                                                                                                                            Ol-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
124c10.10 protein (Hypothetical 52.4 kDa protein)
124c10.10 OR F14c21.51 OR ATIG54990.
Arabidopsis thaliana (Mouse-ear cress)
Eukaryota; Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brasslcales; Brasslcaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                          Federapiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F., Altafi H., Nguyen M., Lam B., Southwick A., Miranda M., Brooks S., Buehler E., Chao Q., Chin C., Chiou J., Choi E., Gonzalez A., Lenz C., Liu A., Liu S., Mukharsky N., Pham P., Sakano H., Shinn P., Toriumi M., Vaysberg M., Yu G., Ecker J., Theologis A., Shinn P., Submitted (AUG-2000) to the EMBL/GenBank/DbBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16.5%; Score 84; DB 10; Length 473; 36.8%; Pred. No. 0.34; Live 10; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
SEQUENCE 473 AA; 52419 MW; D09124A11565BB23 CRC64;
                                                                                                                        473 AA.
                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 408:816-820(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 36.89 nes 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                    RES.
09FZ33
- 09FZ33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                               RESULT 12
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RY STAINTHEEREKLERY,
RA Admars M. D., Celinker S. E., Holt R. A., Evans C. A., Gocayne J. D.,
RA Admars M. D., Celinker S. E., Holt R. A., Eshans R. A., Galle R. F.,
RA George R. A., Lewise S. E., Holt R. A., Eshans R. A., Galle R. F.,
RA Manaticles P. G., Scherer S. E., LI P. W., Hoskins R. A., Galle R. F.,
RA George R. A., Lewise S. E., Holt R. A., Sabburner M., Henderson S. N.,
RA Sutton G. G., Wortman J. R., Yandell M. D., Zhang O., Chen L. X.,
RA Barlaw R. M., Doyle C., Baxer E. G., Helt G., Nelson C. R., Miklog G. L. G.,
RA Ballew R. W., Basu A. Baxendale J., Bayraktaroglu L., Beasley E. N.,
RA Beeson K. Y., Benes P. V. Berman B. P., Bardart D., Ballahakov S.,
RA Borkova D., Botchan M. R., Bouck J., Brokstein P., Barottler P.,
RA Gery J. M., Cawley S., Dallke C., Davenport L. B., Davies P. Chery J. M., Cawley S., Dunkov B. G., Dunn P.,
RA Gery J. M., Cawley S., Dallke C., Davenport L. B., Davies P.
RA Godson K. Doup L. E., Downes M., Dugan-Rocha S., Pleistofhman W.,
RA Godson K. Doup L. E., Downes M., Dugan-Rocha S., Pleistofhman W.,
RA Harris N. L., Harvey D., Helman T. J., Hernandez J. R., Hostin D., Hall M., Ralush F., Karpen G. H., Re Z., Kennison J. A., Ketchum R.A.,
RA Hostin D. Houston K. A., Howland T. J., Wei M.-H., Ibeyam C.
A Jalali M., Kalush F., Karpen G. H., Re Z., Kennison J. A., Ketchum R.A.
Liu X., Mattei B., Morincsh T. C., McLeod M. P., Moshrefi A.,
Murphy B., Murphy B., Murphy B., Morherson D.,
R. Alason P., Leit Y., Levitsky A.A., Li J., Liang Y., Lin Z.,
R. Alason D. R., Nelson K.A., Mixon K., Musskern D.R., Pacled J. M.,
R. Spier E., Standing A.C., Stunders R., Wen Gasenben J.,
R. Spier E., Standing A.C., Stunders R., Wen S., Pollard J., Pollard J., Wan R., Wassarman D.A., Weinstoon M., Strong R., Wassarman D.A., Weinstoon M., Wener J. C.,
R. The Genome sequence of Drosophila melanogaster. T.,
R. Plessen FBannolsself C., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŝ
409 DYISEFV-SLLPKSIRR----VAEEPIPEEVQKVLEEAKAGDDHDHHHGHGHAHAGY 460
                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1561 AA; 174616 MW; 10BFD38A3DD4FC4E CRC64;
                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                       PRT; 1561 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FlyBase; FBgn0025864; Crag.
InterPro; IPR005112; dDENN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; IPR005113; uDENN.
                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001194; DENN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF03455; dDENN; 1. Pfam; PF02141; DENN; 1. Pfam; PF03456; uDENN; 1.
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                     Ephydroldea; Dros
NCBI_TaxID=7227;
                                                                                                                                                                                                      CRAG protein.
CRAG OR CG12737.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                     Q9W3D2
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Matches 2
                                                           RESULT 13
09W3D2
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Matches

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Celniker
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     SORRE
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RA Addam N. Celniker S.E., 11 P.W., Hoskins R.A., Galle R.F.,
Andama N.D. Celniker S.E., 11 P.W., Hoskins R.A., Galle R.F.,
Andama N.D. Celniker S.E., Richards S., Ashburner M. Henderson S.N.,
George R.A., Lewis S.E., Richards S., Ashburner M. Henderson S.N.,
B. Sutton G.G., Worthan J.R., Yandell M.D., Zhang Q., Chen L.X.,
R. Brandon R.C., Baxter E.G., Helt G., Champe M., Pfeliffer B.D.,
R. April J.F., Agbayani A., An H. J., Andrews Pfannkoch C., Baldwin D.,
R. Ballew R.M., Basu A., Baxendale J., Bayraktarioju L., Basalay E.M.,
B. Ballew R.M., Basu A., Bandled J., Bayraktarioju L., Beaslay E.M.,
R. Ballew R.M., Basu A., Bouck J., Brokatin D., Bolshakoy S.,
B. Delchan M.R., Bouck J., Brokatin D., Bolshakoy S.,
B. Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
B. Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
B. Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
B. Burtis R., Dough E.S., Downes M., Down I., Dow I., Dietz S.M.,
R. Burtis K.C., Busam D.A., Buller H., Gu Z., Mays A.D., Dow I., Dietz S.M.,
R. Burtis K.C., Busam D.A., Buller H., Gu Z., Reriaz C., Ferriara S., Fleischmann W.,
R.A. Dougon F., Correll J.H., Gu Z., Gaun P., Raris M.,
R. Douston K.A., Howland T.J., Wei M.H., Ibeywam C.,
R.A. Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
R.A. Mantel B.E., Kodirac C.D., Kratic C., Kravitz S., Kulp D., Lai Z.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.L.
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.K.,
R. Melson D.R., Nelson K.A., Moyler J.C., Scheeler F., Shen H.,
R. Shee E., Spanding A.C., Stapleton M., Strong R., Weiner E., Spanding A.C., Stapleton M., Strong R., Weiner E., Spanding T. S., Wholley K., Weiner E., Spanding T. S., Wholley K., Weiner E., Spanding T., Shong F., Nosher B., Shong T., Wolder J.C., Scheeler F., Shen H., Well S., Shong T., Shong R., Weilber S., Weil M., Weiler B., Shong T., Shong F., Shong T., Shong T., Shong T., Shong T., Shong T., S
                            47
                                                                                        Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota: Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRIN-BERKELEY;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
                                                                     48 GANH-----HHHHGHHGGHGFVVRE------TRVEEDINTCTGEVHERRES
                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                             168 AA
                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly).
              12 EEVRSVAPAGFGRHGGGVQQ-----
                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-BERKELEY;
MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 287:2185-2195(2000)
                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLEEL. 13,
01-MAY-2000 (TREMBLEEL. 13,
01-JUN-2002 (TREMBLEEL. 21,
                                                                                                                                                                                                                                                                           CG7406 protein (RE04580p).
                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                Q9VWM5
                                                                                                                                                                                                Q9VWM5
                                                                                                                                                               RESULT 14
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3 YYQEVDYCSEEVRS---VAPAGFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHHHHHGHHG 59
                                                                                                                                                                                                                                         46 VKVISEE-----AGHGGWAGGYSGGYAH-APEEVKIVKVISEAGHSHGHDYGHSHGHGS 98
                                                                                                                                                                                                              7 VDYCSEEVRSVAPAGFGRHGGGVQ---QHVVKEKFEEVDTVSRAGANHHHHHHHHGHHGGHGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Petromyzon marinus (Sea lamprey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Force A. Amores A., Postlethwait J.;
Force A., Amores A., Postlethwait J.;
Force Juster organization in the jawless vertebrate, Petromyzon
marinus, and the evolution of the vertebrate Hox clusters.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AY056469; AAL17914..;
InterPro; IPR001825; Antennapedia.
InterPro; IPR001835; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3;
                                                                                                                                                                         10;
                                                                                                                              16.3%; Score 83; DB 5; Length 168; 32.9%; Pred. No. 0.13;
Live 9; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
    to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 381 AA; 43860 MW; 4FD20E59DC48E636 CRC64;
(TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16.2%; Score 82.5; DB 13;
29.0%; Pred. No. 0.38;
Live 9; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Petromyzontiformes; Petromyzontidae; Petromyzon
                                                                                                                                                                                                                                                                                                                                                                                                                                                           381 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00032; ANTENNAPEDIA; UNKNOWN_1.
PROSITE; PS00027; HOMEOBOX_1; UNKNOWN_1.
PROSITE; PS50071; HOMEOBOX_2; 1.
HOMEOBOX; Nuclear protein.
NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homeobox protein hox4x (Fragment).
                                                                                                                                                                                                                                                                                                                                                   99 DVKIIKVIQEEGHSHGHGH 117
                                                                                                                                                                                                                                                                                                          64 VVRETRVEEDINTCTGEVH 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProDom; PD000010; Homeobox;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00046; homeobox; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 16.2's
Best Local Similarity 29.0's
Matches 18; Conservative
                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: June
Job time : 51 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                          Query Match
Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=7757;
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01-DEC-2001 (
01-MAR-2002 (
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

June 6, 2003, 12:48:33 ; Search time 25 Seconds (without alignments) 357.620 Million cell updates/sec Run on:

US-10-090-035-4 510 1 MAYYQEVDYCSEEVRSVAPA......INTCTGEVHERRESFLARAN 93 Perfect score:

Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

283224 Total number of hits satisfying chosen parameters: 283224 seqs, 96134422 residues

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_73:\*
1: pirl:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description			TINY-like protein	delta/YY1/NF-E1/UC	related to multifu	hypothetical prote		hypothetical prote	glycine/proline-ri	transcription fact	hypothetical prote	abscisic acid-and	environmental stre	hypothetical prote	protein corA, cold		Down-syndrome-crit	hypothetical prote					transforming prote		dve protein - frui	9	,		-	Zinc tinger bindin hypothetical prote
SUMMARIES	σı	288426	140	A48273	2007	43010	76670	7000	T40009	211109	T16431	11043/	44004	00000	10038	109092	0000	27428	T.104.36	78050	STICE	100080	OTION	TVFVAF	F/1434	TOOT.	T13717	T26757	T16435	JC7089	3594
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	h DB																									7 (	~	~	~	~	7
	Length	6	25.	41,	124	471	47	7.2	172	4 4	à	5	3.5	1272	207	414	757	, ,	333	9 6	15.6	7.00	9 4	2 0	200	5:	φ,	410	83	89	1891
æ	Query		æ	8	~	17.0	· 6				ഗ	15.9	S					15				. 4	•				•	٠	٠	٠	14.5
	Score	92.5	N	92	8	86.5	84	82.5	8	81.5	81	81	80	80	79	79	77	ω.	76.5	7	76	75.5		7.5	7.5	2 6	, , ,	; '	4	74	74
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hypothetical prote probable AT-hook D hypothetical prote gamm-aminobutyric serine/threonine-s hypothetical prote hopothetical prote hopothetical prote hopophopyruwate hy phosphopyruwate hy histidine rich cal hypothetical prote cation efflux fami female sterile hom kakapo gene protei environmental stre
T16440 E84766 S09880 S09880 A202702 A26030 A26030 A26030 A56446 A56466 A56466 A56466 A56466 A56466 A574111111111111111111111111111111111111
ппопопопопопопо
147 285 499 499 606 635 1585 1585 268 499 338 2038 2396 59
4444WWUH000WWWW
144.4 144.4 144.4 144.3 144.0 113.9 113.9 113.9
73.5 73.5 73.5 73.5 72.5 72.5 71.5 71.5 71.5 71.5 71.5 71.5
0 6 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8

## ALIGNMENTS

Cold Sp

RESULT 2

TS2013
TS2013
TS2013
TS2013
TS2019
TINY-like protein [imported] - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 24-Oct-2000 #sequence\_revision 24-Oct-2000 #text\_change 24-Oct-2000
C;Accession: T52019
R;Terryn. N.; Hellinen, L.; De Keyser, A.; Van Asseldonck, M.; De Clercq, R.; Verbakel R;Terryn. N.; Hellinen, E.; De Keyser, A.; Van Montagu, M.; Rouze, P.; Vos, P. A;Title: Exidence for an ancient chromosomal duplication in Arabidopsis th aliana by A;Reference number: 226022; MUID:99192287; PMID:10094464
A;Reference number: Z26022; MUID:99192287; PMID:10094464
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-259 <-TER>
A;Residues: 1-259 <-TER>
C;Genetics:
A;Map position: 4

Query Match

18.1%; Score 92.5; DB 2; Length 259;

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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, C.; Alon R;Theologis, A.; Ecker, J.R.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Hulzar, L.; Januture 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, A;Authors: Hill, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shino, P.; Southwick, A.M.; Sun, H.; Tallo A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MuID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; Pauley, A.; Scheet, P.; Harper, M.
R; Pauley, A.; Scheet, Data library, February 1999
submitted to the EMBL Data library, February 1999
A; Description: The sequence of C. elegans cosmid W03G1.
A; Reference number: Z21454
A; Accession: T3397
A; Accession: T3397
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-471 <-Pauly
A; Residues: 1-471 <-Pauly
A; Ctoss-references: EMBL:AF125964; PIDN:AAD14753.1; GSPDB:GN00022; CESP:W03G1.5
A; Ctoss-references: strain Bristol N2; clone W03G1
A; Genetics: A; Genetics: A; Genetics: A; Map position: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein T24C10.10 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar_2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein W03G1.5 - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C.Accession: T33997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----GVQQHVVKEKFEEVDTVSRAGANHHHHG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 471;
A;Molecule type: DNA
A;Residues: 1-1245 <SCH>
A;Cross-references: EMBL:AL356815; GSPDB:GN00116; NCSP:B24H17.10
A;Experimental source: BAC clone B24H17; strain OR74A
                                                                                                                                                                                                                                                    Length 1245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16; Indels
                                                                                                                                                                                                                                                                                                              3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 86.5; DB 2;
Pred. No. 0.14;
4; Mismatches 16;
                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                        0.21;
                                                                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                             Score 89;
Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                   918
                                                                                                                                                                                                                                                                                                                                                                          SRAGANHHHHHHGHG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17.0%;
nilarity 34.8%;
Conservative 4
                                                                                                                                                                                                                                                          Query Match 17.5%;
Best Local Similarity 72.2%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           15 RSVAPAGFGRHGG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        РРННСННИЕ 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-473 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
nes 24; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
                                                                                                                              C; Genetics:
A; Gene: NCSP:B24H17.10
                                                                                                                                                                                        A; Map position: 6
A; Introns: 6/2; 1141/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22
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C;Species: Neurospora crassa
C;Species: Neurospora crassa
C;Species: Neurospora crassa
C;Accession: T49815
R;Schulte, U; Aign, V; Hoheisel, J; Brandt, P; Fartmann, B; Holland, R; Nyakatura, R;Schulte, U; Aign, V; Hoheisel, May 2000
A;Reference number: Z25022
A;Accession: T49815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: MRNA
A; Molecule type: MRNA
A; Molecule type: MRNA
A; Residues: 1-414 < FLDA
A; Cross-references: GB: M73963; NID: 9202270; PIDN: AAA40522.1; PID: 9202271
A; Cross-references: GB: M73963; NID: Backbone (NCBIN: 74641, NCBIP: 74642)
A; Cross-reference extracted from NCBI backbone (NCBIN: 74641, NCBIP: 74642)
B; Note: sequence extracted from NCBI backbone (NCBIN: 74641, NCBIP: 74642)
B; Note: sequence extracted from NCBI backbone (NCBIN: 74641, NCBIP: 74642)
B; NCBIP: NCBIP: NCBIP: NCBIP: NCBIP: 746404
A; Reference number: A56418
A; Accession: A56418
                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 01-Dec-2000
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 01-Dec-2000
C;Accession: A48273; A42055; A56418
R;Safrany, G.; Perry, R.P.
R;Safrany, G.; Perry, R.P.
A;Title: Characterization of the mouse gene that encodes the delta/YY1/NF-E1/UCRBP trans
A;Title: Characterization of the mouse gene that encodes the delta/YY1/NF-E1/UCRBP trans
A;Reference number: A48273; MUID:93296177; PMID:8516301
A;Accession: A48273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Cross-references: GB:L13968; NID:9293847; PIDN:AAA40477.1; PID:9293849
A, Cross-references: GB:L13968; NID:9293847; PIDN:AAA40477.1; PID:9293849
B; Flanagan, J.R.; Becker, K.G.; Ennist, D.L.; Gleason, S.L.; Driggers, P.H.; Levi, B.Z.;
Rol. Cell. Biol. 12, 38-44, 1992
A; Title: Cloning of a negative transcription factor that binds to the upstream conserved A; Reference number: A42055; MUID:92107191; PMID:1309593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86
                        5;
                                                                                                               21 GFGRHGGG-VQQHVVKEKFEE----VDTVSRAGA---NHHHHHGH-HGGHGFVVRET--R 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 1-218,'S',220-374,'G',376-414 <HAR>
A;Cross-references: GB:M74590; NID:g192940; PIDN:AAA37521.1; PID:g192941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18.0%; Score 92; DB 2; Length 414; ilarity 31.0%; Pred. No. 0.031; Conservative 7; Mismatches 26; Indels
                                 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                     delta/YY1/NF-E1/UCRBP transcription factor - mouse
         0.016;
            Pred. No. 0.01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Introns: 227/1; 281/2; 301/3; 354/3
C; Keywords: transcription factor; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Status: translated from GB/EMBL/DDBJ
            Best Local Similarity 33.8%; Pre
Matches 24; Conservative 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----HSSSSSHGSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99 VННИОЕVILVO 109
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                                                                                                                                                                                                                                                                   222 INDDLMECSSK 232
                                                                                                                                                                                                             70 VEEDINTCTGE 80
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hes 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-414 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: A42055
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                 RESULT 3
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us-10-090-035-4.rpr

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hypotherical protein F53A9.6 - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C; Accession: T16437
R; Miller, N.
R; Miller, N.
B; Mille
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transcription factor Brn-1 - mouse

N;Alternate names: class III POU domain protein brain-1

C;Species: Mus musculus (house mouse)

C;Decte: 02-Dec-1993 #sequence_revision 01-Sep-1995 #text_change 22-Jun-1999

C;Accession: S31223

R;Hara, Y.; Rovescalli, A.C.; Kim, Y.; Nirenberg, M.

Proc. Natl. Acad. Sci. U.S.A. 89, 3280-3284, 1992

A;Tille: Structure and evolution of four POU domain genes expressed in mouse brain.

A;Reference number: S31223

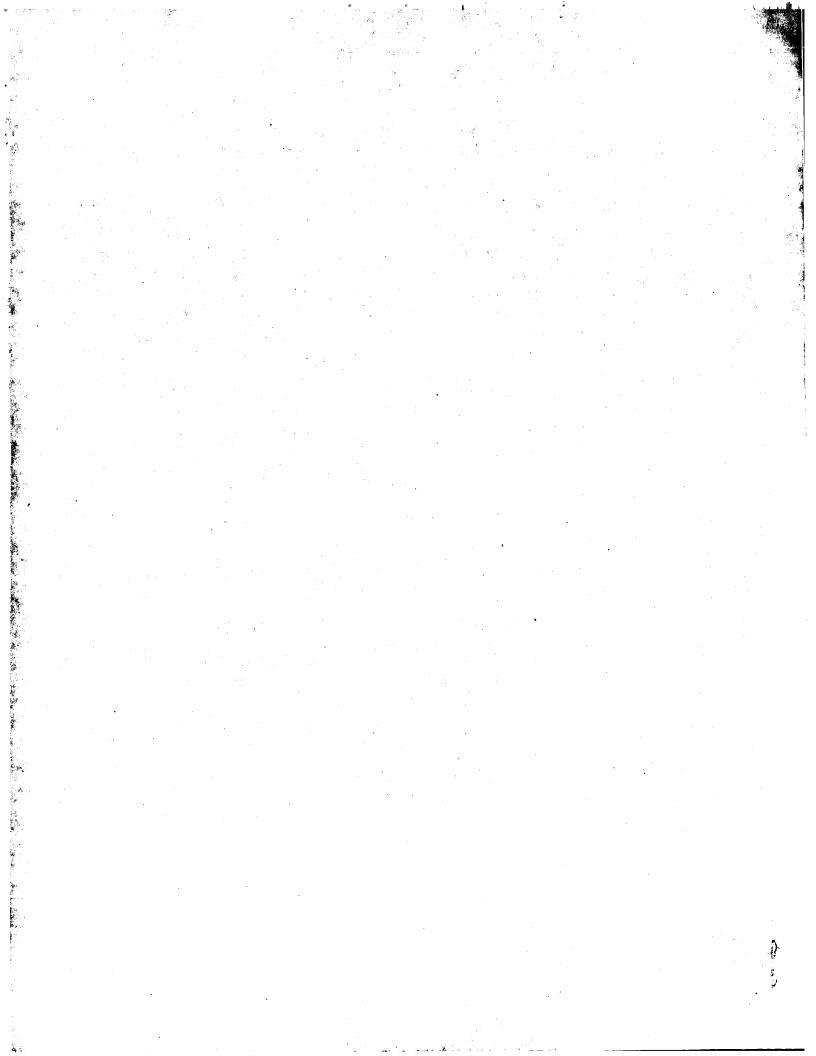
MUD:92228768; PMID:1555520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary
A; Modecule type: DNA
A; Residues: 1-495 - CHARA
A; COSS-references: EMBL: M88299; NID: 9200444; PIDN: AAA39960.1; PID: 9200445
C; Superfamily: transcription factor Brn-1; homeobox homology; POU domain homology
C; Keywords: DNA binding; homeobox; nucleus; transcription regulation
C; Keywords: DNA binding; homeobox; nucleus; transcription regulation
F; 101-112/Region: alanine-rich
F; 102-180/Region: histidine/proline-rich
F; 236-247/Region: plysine-rich
F; 236-247/Region: histidine/proline-rich
F; 2402-391/Region: histidine/proline-rich
F; 2402-921/Region: histidine/proline-rich
F; 2402-458/Domain: homeobox homology <-HOX>
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                                                                                                                                                           Gaps
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                                                                                                                                                  10;
                                                                                                                                                                                                                                                               25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26;
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                                                                                                                                                                                                         19 PAGFGRHGGGVQQHVVKEKFEEVDTVSRAGA----NHHHHGHHGGHGF
                                                                       Length 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                              15;
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                                                              Score 82; DB 2;
Pred. No. 0.15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 PAGFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHH-
                         16.1%; Sco...
34.7%; Pred. No. v...
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      297 GPGLNSHDPHSDEDTPTSDDLEQFAKQFKQRR 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 -----FVVRETRVEEDINTCTGEVHERR 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
16.0%; Score 81.5; Di
Best Local Similarity 26.1%; Pred. No. 0.5;
Matches 24; Conservative 7; Mismatches
                                              Query Match
Best Local Similarity 34.77
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 15.9
Best Local Similarity 29.5
Matches 23; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein Y39B6B.gg [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C;Accession: T45G39
C;Accession: T45G39
Fwilson: R.; Ainscouph, R.; Anderson, K.; Baynes, C.; Berks, M.; Bonfield, J.; Burton, B.; O'Callaghan, M.; Gardner, A.; Green, P.; Hawkins, T.; Hillier, L.; Jier, M.; Johns Bu; O'Callaghan, M.; Parsons, J.; Percy, C.; Rifken, L.; Roopra, A.; Saunders, D. A;Authors: Shownkeen, R.; Sims, M.; Smaldon, N.; Smith, A.; Smith, M.; Sonnhammer, E.; Stack, L.; Wilkinson-Sproat, J.; Wohldman, P.
A;Reference number: S43531; MUID:94150718; PMID:7906398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycine/proline-rich protein - Arabidopsis thaliana
M:Alternate names: protein K10A8_130
C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
B:Sato, S: Nakamura, Y:; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S:; Mex-Accession: T51469
A:Reference number: 225394
A:Reference number: 225394
A:Reference number: 225394
A:Molecule type: DNA
A:Molecule type: DNA
A:Residues: 1-173 <-SAT>

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A;Cross-references: GB:AE005173; NID:99857523; PIDN:AAG00878.1; GSPDB:GN00141
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                                                                                                                                                                                                                                                                                                                      8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43;
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                                                                                                                                                                                                                              DB 2;
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A:Molecule type: DNA
A:Residues: 1-735 <WIL>
                                                                                                                                                                                                             16.5%; Score 84; DB 2;
36.8%; Pred. No. 0.26;
tive 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 82.5; DB Fred. No. 0.6; 1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:AL132896; NA:Experimental source: clone Y39868 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 26.4%;
Matches 19; Conservative
                                                                                                                                                                                                         Ouery Match
Best Local Similarity 36.8%
Matches 21; Conservative
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A;Introns: 18/1; 69/1
A;Note: Y39B6B.gg
                                         C;Genetics:
A;Gene: T24Cl0.10
A;Map position: 1
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A; Introns: 97/1
A; Note: K10A8_130
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Transcription repressor protein YX1 - human NA1ternate names: transcription repressor/activator protein NF-E1 NA1ternate names: transcription repressor/activator protein NF-E1 C; Species: Homo Sapiens (man) C; Species: Homo Sapiens (man) C; Species: Homo Sapiens (man) Sapiens (man) Species: Taul-1992 #sequence_revision 17-Jul-1992 #text_change 08-Oct-1999 C; Accession: A40350; S78494; S33712; A56419 R; Shi, Y; Seto, E; Chang, L.S.; Shenk, T. R; Shi, Y; Seto, E; Chang, L.S.; Shenk, T. Species (F) 377-388 (man) Tepression by XY1, a human GLI-Krueppel-related protein, and A; Reference number: A40350; MUID:92005716; PMID:1655281
                                                                                                                                                                                  The comp
                                                                                                          Nomura, N.; Ohara,
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C;Species: Homo sapiens (man)
C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000
C;Accession: T00338
R;Nagase, T.; JShikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.;
R;Nagase, T.; JShikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.;
R;Nagase, T.; JShikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.;
A;Title: Prediction of the coding sequences of unidentified human genes. IX.
A;Reference number: 214086; MUID:98290545; PMID:9628581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein cora, cold- and drought-regulated - alfalfa
C;Species: Medicago sativa (alfalfa)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Residues: 1-204 <LAB>
A; Residues: 1-204 <LAB>
A; Cross-references: EMBL:L03708; NID:g289122; PIDN:AAA99833.1; PID:g289123
C; Genetics:
A; Genetics:
C; Superfamily: Arabidopsis glycine-rich protein 3
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A;Residues: 1-414 <SHI>
A;Cross-references: GB:M77698; NID:g186767; PIDN:AAA59467.1; PID:g186768
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 1273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48 GANHHHHHHHHGHHGGH--GFVVRETRVEEDINTCTGEVHERRESFLA 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19; Indels
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R; Laberge, S.; Castonguay, Y.; Vezina, L.P.
Plant Physiol. 101, 1411-1412, 1993
A; Title: New cold and drought-regulated gene from Medicago
A; Reference number: Z16754; MUID:94143496; PMID:8310076
A; Accession: T09592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary; translated from GB/EMBL/DDBJ
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C;Superfamily: human hypothetical protein KIAA0570
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9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 80;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.7%;
Local Similarity 33.3%;
Les 15; Conservative
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A; Residues: 1-204 <LAB>
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C. Species: Medicago sativa (alfalfa)
C. Species: Medicago sativa (alfalfa)
C. Species: Medicago sativa (alfalfa)
C. Species: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 02-Jun-2000
C. Accession: 109608
R. Luo, M.; Mohapatra, S.; Hill, R.
submitted to the EMBL Data Library, February 1992
A. Boscription: Nucleotide sequence analysis of a environmental stress and ABA inducible A; Reference number: 216770
A. Accession: T09608
A. Accession: T09608
A. Accession: T09608
A. Molecule type: mRNA
A. Residues: 1-133 < LUO>
                                                                                                                                                                                                                                                                                                                                                                               abscist acid-and environmental stress-inducible protein - alfalfa (fragment)
C;Species: Medicago sativa (alfalfa)
C;Species: Medicago sativa (alfalfa)
C;Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C;Accession: A42844
R;Luo, M.; Liu, J.H.; Mohapatra, S.; Hill, R.D.; Mohapatra, S.S.
J; Biol. Chem. 267, 15367-15374, 1992
A;Title: Characterization of a gene family encoding abscisic acid- and environmental str
A;Reference number: A42844; MUID:92348382; PMID:1379227
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                                  |:|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| |
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NCBIP:109889)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-191 <LUO>
A; Cross-references: GB:S40947; NID:g252396; PIDN:AAB22713.1;
A; Cross-references: GB:S40947; NID:g252396; PIDN:AAB22713.1;
A; Note: sequence extracted from NCBI backbone (NCBIN:109886,
C; Superfamily: Arabidopsis glycine-rich protein 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross references: EMBL:W74190; NID:g166373; PID:g166374 A; Experimental source: cultivar Anik C; Superfamily: Arabidopsis glycine-rich protein 3
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Pred. No. 0.18;
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Best Local Similarity 28.7%; Pred. No. 0.18
Matches 27; Conservative 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 81; DB Pred. No. 0.213; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGHGGHGGHGADQTEDNTQNDHN 175
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                                                                                                                                                                                                 ::|| || |||||||| 52 ННDSHHRGGHHGGH 69
                                                                                                                                                   46 RAGANHH--HHHGHHGGH 61
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30.1%;
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Best Local Similarity 30.1°
Matches 25; Conservative
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A; Status: preliminary
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A; Experimental source: HeLa cells
A; Note: the authors translated the codon CGC for residue 371 as Lys, CGA for residue 375
R;Whitson, R.H.; Huang, T.; Dang, J.; Itakura, K.
Bubmitted to the EMBL Data Library, July 1992
A; Description: Observed and predicted DNA binding of a zinc finger protein which recognial A; Reference number: S78494
A; Reference number: S78494
A; Reference number: A; Reference number: By Reference numbe
                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Modecule type: mRNA
A; Residues: 1-195, 'G', 197-414 <WHI>
A; Residues: 1-195, 'G', 197-414 <WHI>
A; Cross-references: EMBL: 214077; NID:938010; PIDN:CAA78455.1; PID:938011
A; Cross-references: EMBL: 214077; NID:9808, 1991
Broc. Natl. Acad. Sci. U.S.A. 88, 9804-9808, 1991
A; Title: Isolation of a candidate repressor/activator, NF-E1 (YY-1), delta, that binds A; Reference number: A56419; MUID:92052179; PMID:1946405
A; Accession: S33712
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A; Residues: 1-64, R', 66-195, 'G', 197-414 <PAR>
A; Residues: 1-64, R', 66-195, 'G', 197-414 <PAR>
A; Cross-references: GB:M76541; NID:g189173; PIDN:AAA59926.1; PID:g189174
C; Reywords: DNA binding: transcription regulation; zinc finger
F; 298-320/Region: zinc finger CCHH motif
F; 357-347/Region: zinc finger CCHH motif
F; 385-407/Region: zinc finger CCHH motif
F; 385-407/Region: zinc finger CCHH motif
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Pred. No. 0.78;
6; Mismatches 25; Indels
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Best Local Similarity 29.2%;
Matches 21; Conservative
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Search completed: June 6, 2003, 12:53:25 Job time : 26 secs



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Sequence 3, Application US/10090035
Sequence 3, Application US/10090035
Sequence 3, Application US/10090035
Sequence 3, US2002017008941
SERENT INFORMATION:
TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible
TITLE OF INVENTION: Proteins and Uses Thereof
FILE REFERENCE: 35718/24990
CURRENT APPLICATION NUMBER: US/10/090,035
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 60/272,227
PRIOR APPLICATION NUMBER: 60/272,227
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93
US-09-738-973-43

US-10-291-737-3

US-10-291-737-3

US-09-738-626-1

US-10-103-313-83

US-10-103-313-83

US-10-103-313-83

US-09-884-60-1

US-09-984-130-143

US-09-984-130-143
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Matches:
Conservative:
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US-09-918-995-6480
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US-10-052-798-7
US-10-278-173-15
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US-10-090-035-3
                                  TYPE: DNA
ORGANISM: Zea mays
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Percent Similarity:
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LOCATION: (96
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US-10-090-035-3
499.5
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 Command line parameters:

-WODEL-frame+_p2n.model -DEV-x1h
-O-Cgn2_1/USFO_2-p001/US10090015/runat_06062003_105507_11116/app_query.fasta_1.526
-O-Cgn2_1/USFO_2-p001/US10090015/runat_06062003_105507_11116/app_query.fasta_1.526
-DB=Published_Applications_NA -OFMT-fastap -SUFFIXT-rnpb -MINARTCH-0.1
-LOOPCL-0 -LOOPEXT-0 -UNITS-bits -START-1 -END--1 -MATRIX-blosum62
-TRANS-human40.cd1 -LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MAX-100
-MAXLEN-2000000000 -USER-US10090035_eCGN_1_1_176_erunat_06062003_105507_1116
-NCPU-6 -ICPU-3 -NO_MMAP -LARGEQUERY -NGG_SCORES=0 -WAIT -DSPBLCCK-100
-LONGLOG -DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS=1 -XGAPOP=10 -XGAPEXT-0.5
-FGAPOP-6 -FGAPEXT-7 -YGAPOP=10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7
                                                                                  (without alignments)
1077.357 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Sequence 5, Sequence 1, Sequence 1, Sequence 9, 1
                                                                                                                                  1 MAYYQEVDYCSEEVRSVAPA.....INTCTGEVHERRESFLARAN
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1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/DCC_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
5: /cgn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
7: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
7: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
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11: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
12: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
12: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
                                                                June 16, 2003, 11:41:43; Search time 125 Seconds
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  GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
                                            nucleic search, using frame_plus_p2n model
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                                                                                                                                                                                                                          1029858 seqs, 724030393 residues
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US-10-090-035-5
US-10-090-035-1
US-10-090-035-9
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Maximum DB seq length: 2000000000
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Squence 9, Application US/10090035
Paquence 9, Application US/10090035
Patent No. US200201700891
GENERAL INFORMATION:
APPLICANT: Simmons, Carl R.
TITLE OF INVENTION: Proteins and Uses Thereof
FILE REPRENCE: 35718/24290
FILE REPRENCE: 35718/24290
CURRENT APPLICATION NUMBER: US/10/090,035
CURRENT APPLICATION NUMBER: 05/272,227
                                                                                                Sequence 1, Application US/10090035
Patent No. US20020170089A1
GENERAL INFORMATION:
APPLICANT: Simmons, Carl R.
APPLICANT: Simmons, Carl R.
TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible TITLE OF INVENTION: Proteins and Uses Thereof
FILE REFERENCE: 35718/242990
CURRENT APPLICATION UNMBER: US/10/090,035
CURRENT FILING DATE: 2002-02-28
PRIOR PILING DATE: 00/28/2001
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                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 676
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Best Local Similarity:
Query Match:
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ORGANISM: Zea mays
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WESULY 1.

WESULY 1.

Sequence 5, Application US/10090035

Sequence 5, Application US/10090035

Sequence 6, US20020170089A1

SEQUENCE 1 US20020170089A1

SEQUENCE 6, US20020170089A1

TITLE OF INVENTION: No.1eic Acids Encoding Defense Inducible TITLE OF INVENTION: Proteins and Uses Thereof

TITLE OF INVENTION: Proteins and Uses Thereof

TITLE OF INVENTION: Proteins and Uses Thereof

CURRENT APPLICATION NUMBER: US/10/090,035

CURRENT FILING DATE: 2002-02-28

SETOR PAPLICATION NUMBER: 60/272,227

PRIOR FILING DATE: 20/2/28/2001

NUMBER OF SEQ ID NOS: 25

SEQ ID NO 5

LENGTH: 577
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Matches:
Conservative:
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                                                         US-10-090-035-4 (1-93) x US-10-090-035-3 (1-574)
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; LOCATION: (99)...(377)
US-10-090-035-5
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Best Local Similarity:
Query Match:
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              Best Local Similarity:
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                          Query Match:
DB:
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	. YO	1	MetAlaTy	rTyrG	InGluValAs	pTyrCysSerGluGlu	MetalaTyrTyrGlnGluValaspTyrCysSerGluGluValArgSerValAlaProAla	20
	සු	57	ATGGCTTA	CTACC	AGGAGGTGGA	CTACTGCTCGGAGGAG	sranderceereeccceecc	116
	oy Db	21	GlyPheGl	yArgh        cccc	18GlyGlyGly 	yValGlnGlnHisValvelvelvelvelvelvelvelvelvelvelvelvelvel	GlyPheGlyArgH1sGlyGlyClyValGlnGlnH1sValValLysGluLysPheGluGlu 	40
	ν	41	ValAspTh	rvals	erAraAlagi	AlakanHisHis	dientendentunt outon)	
	qa	177	GECGACAC	GGTCT	CACGCGCCGG	GCCAACCACCACCACCACCACCACCACCACCACCACCACC		236
	δο d	933	GlyHisGl	yPhev 	alvalArgGlu	ThrargvalGluGlu	GlyHisGlyPheValValArgGluThrArgValGluGluAspIleAsnThrCysThrGly	79
	2 6	/87	GGCCACGG	CTTCG	TGGTGCGCGAC	BACCAGGGTCGAGGAGG	CATCAACACCTGCACCGGC	396
	දු දි	29.7	GluvalH1 	8G1uA:	rgArgGluSer 	G1uVa1H18G1uArgArgG1uSerPheLeuAlaArgAlaAs 	6 6	
	3	167	GAGGICCA	CGAGC	GCAGGGAGAGG	TTCCTCGCCAGGGCTA	AC 338	
·	RESULT 6 US-10-090 ; Sequenc ; Patent	-035- e 7, No. U	7 Applicat S2002017	10n US 0089A]	RESULT 6 US-10-090-035-7 Sequence 7, Application US/10090035 ; Patent No. US200201700899A1			
	; GENERAL ; APPLIC	INFO ANT:	RMATION: Simmons,	Carl	R.			
	; TITLE	OF IN	VENTION:	Prot	eic Acids E	Encoding Defense Uses Thereof	Inducible	
	CURREN	T APP T FIL	LICATION ING DATE	NUMBE 1200	2990 ER: US/10/090 02-02-28	90,035		
	, PRIOR	APPLI FILIN	CATION NI G DATE: (	JMBER: 02/28/	. 60/272, 22 /2001	7		
	SOFTWA	OF S	EQ ID NO: astSEQ fo	3: 25 or wir	ndows Versi	on 4.0		
	SEQ ID NO 7	ID NO 7	0				•	
		ISM:	Zea mays					
			ro .					
	; LOCATION: US-10-090-035		:	(380)				
	Alignment :	Scores	: 80	20	5-57		Ç	
	Score:	[m1]a		499.	0.0		93	
	Best Local Similar Query Match: DB:	L S1m1 ch:	larity:	99.0	2 4 4 8 8 8	Conservative: Mismatches: Indels: Gaps:	7,000	
	US-10-090	-035-4	4 (1-93)	x us-	-10-090-035	-7 (1-580)		
	οy	-	(etAlaTyr	Tyrel	nGluValAsp	PyrCysSerGluGluV	MetalaTyrTyrGlnGluValaspTyrCysSerGluGluValargSerValalaProAla 2	0
	ОЪ	66	TGGCTTAC	TACCA	GGAGGTGGACT	TACTGCTCGGAGGAGG	GAGGTCGGTGCCCCCGGCC 1	28
	٥y	21 G	31yPheGly	Arghi	sGlyGlyGly	ValGlnGlnH18ValVe	alLysGluLysPheGluGlu 4	0
	QQ	159 6	SCTTCGC	CGCCA	CGGAGGCGGC	STCCAGCAGCACGTCG	7	18
	Qy	41 V	alAspThr	Valse	rArgAlaGlyA	AlaAsnHisHisHi	ValAspThrValSerArgAlaGlyAlaAsnHisHisHisHisGlyHisHisGly 5	σ
	qa	219 G	TCGACACG	GTCTC	ACGCGCCGGCC	SCCAACCACCACCACCA		278
_	οy	9 09	GlyHisGly	Pheva	lvalArgGlu1	ihrArgvalGluGluAs	sGlyPheValValArgGluThrArgValGluGluAspIleAsnThrCysThrGly 7	σ.

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Alignment Scores:
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40 GluvalAspThrValSerArgAlaGlyAlaAsnHisHisHisHisGlyHisHisGly 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 GlyHisGlyPheValValArgGluThrArgValGluGluAspIleAsnThrCysThrGly 79
                                                                                                                                         Sequence 15, Application US/10090035

Sequence 15, Application US/10090035

Patent No. US20020170089a1

GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible
TITLE OF INVENTION: Proteins and Uses Thereof
FILE REFERENCE: 35718/242990;
CURRENT APPLICATION NUMBER: US/10/090,035

CURRENT FILING DATE: 2002-02-28

PRIOR APPLICATION NUMBER: 60/272,227

PRIOR PELING DATE: 20/248/2001

NUMBER OF SEQ ID NOS: 25

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 21, Application US/10090035
Patent No. US20020170089A1
GENERAL INFORMATION:
APPLICANT: Simmons, Carl R.
TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible TITLE OF INVENTION: Proteins and Uses Thereof
FILE REFERENCE: 35718/242990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  292 GAGITCCGCGAGCGCAAGCAGAGCTTCCTGCTCCTAAGTCCGAC 333
                                               80 GluValHisGluArgArgGluSerPheLeuAlaArgAlaAsn 93
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Mismatches:
Indels:
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Matches:
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LOCATION: (61)...(333)
NAME/KEY: misc.feature
LOCATION: (1)...(591)
OTHER INFORMATION: n = A,T,C or
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295.00
75.53%
60.64%
57.84%
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ORGANISM: Oryza sativa
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Best Local Similarity:
Query Match:
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165 CAGGAGTICGACACCTCCGGCCGC------CGCCACGGTCACCACGGTCACCAC 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                        39 GluGluValAspThrValSerArgAlaGlyAlaAsnHisHisHisHisHisGlyHisHis
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Sequence 19, Application US/10090035
Sequence 19, Application US/10090035
Sequence 19, Application US/10090035
Sequence 10, Application US/10090035
TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible TITLE OF INVENTION: Proteins and Uses Thereof TITLE OF INVENTION: UNMER: 2090
CURRENT APPLICATION NUMBER: 60/272,227
PRIOR APPLICATION NUMBER: 60/272,227
PRIOR FILING DATE: 02/28/2001
NUMBER OF SEQ 1D NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
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60
12
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Conservative:
Mismatches:
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                          PRIOR APPLICATION NUMBER: 60/272,227
PRIOR FILING DATE: 02/28/2001
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21
LENGTH: 436
CURRENT APPLICATION NUMBER: US/10/090,035 CURRENT FILING DATE: 2002-02-28
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                                                                                                                                                                ORGANISM: Triticum aestivum
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73.478
61.228
54.418
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NAME/KEY: misc_feature
                                                                                                                                                                                               ; NAME/KEY: CDS
; LOCATION: (54)...(326)
US-10-090-035-21
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OTHER INFORMATION: n
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Best Local Similarity:
Query Match:
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SEQ ID NO 19
LENGTH: 584
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                                                                                                                                                 TYPE: DNA
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us-10-090-035-4.rnpb

Qy       39GludluValAspThrValSerArgAlaGlyAlaAsnHisHisHisHisHisHisBlyHis 57         157 GTGCAGGAGTTCGACACCGCCGCCGCCCCCGCCAYGGTCACCACGGTCAC       204         Qy       58 HisGlyGlyHisGlyPheValValArgGluThrArgValGluGluAspIle 74         11111       111111111111111111111111111111111111	Sequence 13, Application US/10090035 Sequence 13, Application US/10090035 Sequence 13, Application US/10090035 Setcent No. US20020170089A1 SENERAL INFORMATION: APPLICANT: SIMMONS, CAT1 R. APPLICANT: SIMMONS, CAT1 R. APPLICANT: SIMMONS, CAT1 R. TITLE OF INVENTION: Proteins and Uses Thereof FILE REFERENCE: 35718/24299 CURRENT APPLICATION NUMBER: US/10/090,035 PRIOR APPLICATION NUMBER: 02/28/2001 PRIOR FILING DATE: 02/28/2001 NUMBER: OF SED ID NOS: 25 COURTAIN OF THE SECOND OF	SEQ ID NO 13 TYPE: DAR TYPE: DAR ORGANISM: Oryza sativa ORGANISM: Oryza sativa FEATURE: NAME/KEY: CDS LOCATION: (52)(348) NAME/KEY: misc_feature LOCATION: (1)(348) OTHER INFORMATION: n = A,T,C or G S-10-090-035-13 11gnment Scores: 1.39e-24 Len core: 251.00 Mat est Local Similarity: 70.59% Con est Local Similarity: 60.00% Miss est Local Similarity: 60.00% B:	US-10-090-035-4 (1-93) x US-10-090-035-13 (1-348)  QY		80 GluvalHisGluhrg 84                 283 GAGTTCGCGAGCGC 297 SULT 12 -09-923-876-2788 Sequence 2788, Application US/09923876
Pred. No.:  Score:  Score:  Score:  Score:  Percent Similarity:  72.73%  Ratches:  Ratches:  Ratches:  Ratches:  Ratches:  Ratches:  Ratches:  Ratches:  Ratches:  13  Ouery Match:  9.50.59%  Ramatches:  14  Ratches:  15  Ratches:  16  Ratches:  16  Ratches:  16  Ratches:  16  Ratches:  16  Ratch	Oy 20 AlaGlyPheGlyArgHisGlyGlyGlyValGlnGlnHisValValLysGluLysPhe 38	MA SOLL FILL FOR HIS A SOLL FILL FOR HIS FOR H	FEATURE:   FEATURE:   FEATURE:   FEATURE:   FORTION: (46)(321)   FORTION: (46)(321)   FORTION: (1)(584)   FORTION: (1)(584)	Alignment Scores: Pred. No.: 250.00 Score: 250.00 Autohes: Percent Similarity: Best Local Similarity: 50.59 Mismatches: 13 Query Match: 9 10S-10-090-035-4 (1-93) x US-10-090-035-23 (1-584)	Oy 1 MetalaTyrTyrGlnGluValAspTyrCysSerGluGluValArgSerValAlaPro 19

12 24 11 5

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APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
FILE REFERENCE: SCRIP1300-3
                                                                                                                                   | | | | | | | | | ::|||||||||| | ::
328 GGAGGAGGAGTGAACGGTGGAGTATATGTCGCCGCGTATATAAGGAGAAAAAGCGCC 269
                                                                                                                                                                                                           21 GlyPheGlyArgHisGlyGlyGly---ValGlnGlnHisValValLysGluLysPheGlu 39
                                                                                                                  21 GlyPheGlyArgHisGlyGlyGly---ValGlnGlnHisValValLysGluLysPheGlu 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53 HisHisGlyHis---HisGlyGlyHisGlyPheValValArgGluThr----Arg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40 Glu--------AsnHisPThrValSerArgAlaGlyAla------AsnHisHis
                                                                                                                                                                                                                                                       53 HisHisHisGlyHis---HisGlyGlyHisGlyPheValValArgGluThr----Arg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----ValAspThrValSerArgAlaGlyAla-
Conservative:
Mismatches:
Indels:
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Conservative:
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Indels:
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                                                                                US-10-090-035-4 (1-93) x US-09-924-035A-17 (1-328)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/938,842A CURRENT FILING DATE: 2001-08-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRAIN FILING DATE: 2017 00 227, 866

PRIOR FILING DATE: 2000-08-24

PRIOR FILING DATE: 2000-08-24

PRIOR APPLICATION NUMBER: US 60/264,647

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-06-22

NUMBER OF SEQ ID NOS: 5379

LENGTH: 591
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1858, Application US/09938842A Patent No. US20020160378A1 GENERAL INFORMATION:
APPLICANT: Harper, Jeff APPLICANT: Kreps, Joel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana
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50.70%
33.80%
18.14%
50.70%
33.80%
18.14%
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Best Local Similarity:
Query Match:
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Query Match:
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              GENERAL INFORMATION:
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Lalgudi, Laura Y. (Ito)
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
FILE REFERENCE: PL-0012-1 CON
CURRENT PELLING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: 09/298,329
PRIOR APPLICATION NUMBER: 60/085,331
PRIOR APPLICATION NUMBER: 60/085,331
PRIOR FILING DATE: 1998-05-05
NUMBER OF SEQ ID NOS: 6332
SOFTWARE: PERL PROGRAM
SEQ ID NO 2788
LENGTH: 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 ValaspThrValSerArgAlaGlyAlaAsnHisHisHisHisGlyHisHisGlyGly 60
                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Grlach, Jrn
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: thaliana
FILE REFERENCE: 2011US
CURRENT APPLICATION NUMBER: US/09/924,035A
CURRENT FILING DATE: 2000-08-11
PRIOR FILING DATE: 1999-08-13
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 17
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213.00
81.67%
80.00%
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92.50
   Patent No. US20020013958A1
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                          TYPE: DNA
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                                                                                                                                | GENERAL INFORMATION:
| APPLICANT: Friedrich, Glenn
| APPLICANT: Sands, Arthur T.
| TITLE OF INVENTION: No. US20020102543Alel Mutated Mammalian Cells and
| TITLE OF INVENTION: No. US20020102543Alel Mutated Mammalian Cells and
| TITLE OF INVENTION: No. US20020102543Alel Mutated Mammalian Cells and
| TITLE OF INVENTION: Animals
| FILE REFERENCE: LEX-0102-USA
| CURRENT APPLICATION NUMBER: US 60/168,358
| FRIOR FILING DATE: 1999-12-01
| PRIOR FILING DATE: 1999-12-01
| SOFTWARE: FASTSEQ for Windows Version 4.0
| SOFTWARE: FASTSEQ for Windows Version 4.0
| SOFTWARE: Mus musculus
| FEBTURE: MAS MUSCULUS
| FEBTURE: MAS MUSCULUS | FEBTURE: NAME/KEY: MISC_feature
| UCCATION: (1)...(546)
| OTHER INFORMATION: n = A,T,C or G
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Matches:
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RESULT 1  US-10-090-035-2  Sequence 2. Application US/10090035  Patent No. US20020170089A1  GENERAL INFORMATION:  APPLICANT: Simmons, Carl R.  TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible  CURRENT APPLICATION NUMBER: 60/272,227  PRIOR FILING DATE: 2002-02-25  SEQ ID NO 2 25  SEQ ID NO 2 25  SEQ ID NO 2 25  ERNGTH: 93  TYPE: PRT  ORGANISM: Zea mays	67.5 13.2 605 9 US-09-741-233A-2 Sequence 2. 67.5 13.2 1207 9 US-10-108-605.71 Sequence 7. 13.1 446 10 US-09-9853-386-69 Sequence 6. 13.1 507 10 US-09-738-897-2 Sequence 10. 67 13.1 507 10 US-09-738-897-2 Sequence 10. 13.1 507 10 US-09-738-897-2	3 14.3 633 10 US-09-824-735-3 Sequence 3, A	aquence 339 aquence 11, aquence 125, quence 126, quence 129, quence 126, quence 126, quence 126, quence 31, quence 31, quence 21, quence 20, quence 20, quence 10, quence 10, quence 10, quence 20, quence 10, quence 10, quence 10, quence 10, quence 10, quence 10,	Inductible See See See See See See See See See S	3 10 US-09-824-735-3 3 10 US-09-824-735-3 4 10 US-09-927-798-11 2 10 US-10-052-798-11 2 10 US-09-927-798-11 2 10 US-09-927-798-11 3 9 US-10-108-605-125 5 9 US-10-108-605-125 6 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69.5 13.6 623 9 US-10-108-605-125 Sequence 69.5 13.6 628 9 US-10-108-605-129 Sequence 69.5 13.6 726 9 US-10-108-605-129 Sequence 69.5 13.6 257 9 US-09-738-626-6135 Sequence 69.5 13.4 20 US-09-738-626-6135 Sequence 67.5 13.2 138 10 US-09-738-626-6135 Sequence 67.5 13.2 530 9 US-10-044-692-317 Sequence 67.5 13.2 557 9 US-10-044-692-317 Sequence 67.5 13.2 557 9 US-10-044-692-317 Sequence 67.5 13.2 557 9 US-10-044-539-317 Sequence 67.5 13.2 557 9 US-10-070-333-126 Sequence 67.5 13.1 507 9 US-09-741-233, 2.5 Sequence 67.5 13.1 507 9 US-09-78-995-719-201 Sequence 67 13.1 507 10 US-09-75-719-201 Sequence 67 13.1 608 9 US-09-75-719-201 Sequence 67 13.1 643 9 US-09-975-719-199 Sequence 67 13.1 643 9 US-09-975-719-199 Sequence 67 13.1 643 10 US-09-975-719-199 Sequence 67 13.1 643 10 US-09-975-719-199 Sequence 67 13.1 643 10 US-09-975-719-199	69.5 13.6 623 9 US-10-108-605-125 Sequence 69.5 13.6 623 9 US-10-108-605-129 Sequence 69.5 13.6 726 9 US-09-932-2574-19 Sequence 69.5 13.4 20.9 US-09-738-626-6135 Sequence 68.5 13.4 20.9 US-09-601-1013-3 Sequence 67.5 13.2 118 10 US-09-813-820-8 Sequence 67.5 13.2 530 9 US-10-044-692-317 Sequence 67.5 13.2 530 9 US-10-044-539-317 Sequence 67.5 13.2 557 9 US-10-044-539-317 Sequence 67.5 13.2 557 9 US-10-044-539-317 Sequence 67.5 13.2 557 9 US-10-03-317 Sequence 67.5 13.2 557 9 US-10-0	3 14.3 633 10 US-09-824-735-3 Sequence 3.	3, 3,38 11, 501, 11,	. w w w w	ப்பட்டிர் வெள்ளிர்கள்			225 225 26 26 27

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1 MAYYQEVDYCSEEVRSVAPAGFGRHGGGYQQHVVKEKFEEVDTVSRAGANHHHHHGHHGG

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61 HGFVVRETRVEEDINTCTGEVHERRESFLARAN 93  Sequence 4, Application US/10090035
Patent No. US20020170089A1
GENERAL INFORMATION:
APPLICANT: Simmons, Carl R.
TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible
TITLE OF INVENTION: Proteins and Uses Thereof

Sequence 5, App Sequence 2, App Sequence 16, App Sequence 9, App Sequence 10, App

US-10-090-035-4

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US-10-090-035-18
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SEQ ID NO 18
NUMBE: FAST
SOFTWARE: FAST
SEQ ID NO 10
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US-10-090-035-8
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LENGIH: 94
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Sequence 10 US20020170089A1
Sequence 10 US20020170089A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible TITLE OF INVENTION: Proteins and Uses Thereof FILE REPERBNCE: 35718/242990
CURRENT FILING DATE: 2002-02-28
PRIOR PELICATION NUMBER: 60/272,227
PRIOR FILING DATE: 02/28/2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 510; DB 9; Length 93; Best Local Similarity 100.0%; Pred. No. 5e-45; Matches 93; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Simmons, Carl R.

TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible TITLE OF INVENTION: Proteins and Uses Thereof FILE REFERENCE: 35118/242990 CURRENT PRILING DATE: 2002-02-28 PRIOR APPLICATION NUMBER: 60/272,227 PRIOR FILING DATE: 02/28/2001 NUMBER OF SEQ ID NOS: 25 SOFTHARE: 02/28/2001 NUMBER OF SEQ ID NOS: 25 SOFTHARE: FastSEQ for Windows Version 4.0 SEQ ID NO 6 LENGTH: 93
                                                                                                                                                                                                                                                      Length 93;
                                                                                                                                                                                                                                                        Query Match 100.0%; Score 510; DB 9; Length 9 Best Local Similarity 100.0%; Pred. No. 5e-45; Matches 93; Conservative 0; Mismatches 0; Indels
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  FILE REFERENCE: 35718/242990
CURRENT APPLICATION NUMBER: US/10/090,035
CURRENT FILING DATE: 2002-02-28
FRIOR APPLICATION NUMBER: 60/272,227
PRIOR FILING DATE: 02/28/2001
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
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Patent No. US20020170089Al
GENERAL INFORMATION:
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                                                                                                                                                                                    TYPE: PRT; ORGANISM: Zea mays
US-10-090-035-4
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US-10-090-035-6
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CURRENT APPLICATION NUMBER: US/10/090,035
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 60/272,227
PRIOR FILING DATE: 02/28/2001
                                                                                                                    Length 93;
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Pred. No. 5.9e-44;
0; Mismatches 0;
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                                                                                                                    DB 9;
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                                                                                                                    Score 507; DB 9;
Pred. No. 1e-44;
1; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
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Patent No. US20020170089A1
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                                                                                                                                                    92; Conservative
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Best Local Similarity
Matches 93; Conserv
                                                                                                                          Query Match
Best Local Similarity
Matches 92; Conserv
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                                                              ; TYPE: PRT
; ORGANISM: Zea mays
US-10-090-035-10
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13; Gaps

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1 MAYYQEVDYCSEEVRSVA-PAGFGRHGGGVQQHVVKEKF-EEVDTVSRAGANHHHHGHH 58
                                                                         1 MAYYQEVDYCSEEVRSVA-PAGFGRHG-GGVQQHVVKEKF-EEVDTVSRAGANHHHHHGH 57
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Fatent No. US2002017008941
GENERAL INFORMATION:
APPLICANT: Simmons, Carl R.
TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible
TITLE OF INVENTION: Proteins and Uses Thereof
FILE REFERENCE: 35718/24990
CURRENT APPLICATION NUMBER: US/10/090,035
CURRENT APPLICATION NUMBER: 60/272,237
FRIOR FILING DATE: 2002-02-8
FRIOR PRICING DATE: 02/28/2001
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PASSECT for Windows Version 4.0
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TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible FILE REFERENCE: 35718/242990
CURRENT APPLICATION NUMBER: US/10/090,035
CURRENT FILING DATE: 2002-02-28
PRIOR PILING DATE: 02/28/2001
NUMBER OF SEQ ID NOS: 25
SOCTHARE: FastSEQ for Windows Version 4.0
                          13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 53.5%; Score 273; DB 9; Length 92; Similarity 61.6%; Pred. No. 7e-21; 51; Conservative 12; Mismatches 12; Indels
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                                                                                                                         59 G---GHGFVVRETRVEEDINTCTGEVHERRESFLARAN 93
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Patent No. US20020170089A1
GENERAL INFORMATION:
                      12;
                      60; Conservative
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US-10-090-035-20
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Best Local Similarity 58.6%
Matches 58; Conservative
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LENGTH: 92
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LENGTH: 92
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Best Local
                    Matches
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                                                                Length 94;
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TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible FITLE OF INVENTION: Proteins and Uses Thereof CURENT S718/242990 CURRENT FILING DATE: 2002-02-28 CURRENT FILING DATE: 2002-02-28 PRIOR FILING DATE: 02/28/2001 NUWBER OF SEQ ID NOS: 25 SOFTWARE: FastSeq for Windows Version 4.0
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Patent No. US20020170089A1
GENERAL INFORMATION:
APPLICANT: SIMMONS, CATI R.
TITLE OF INVENTION: Proteins and Uses Thereof
FILE REFERENCE: 35718/742990
CURRENT APPLICATION NUMBER: US/10/090,035
CURRENT FILING DATE: 2002-02-28
PRIOR FILING DATE: 0/28/2001
WINDER FILING DATE: 0/28/2001
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Best Local Similarity 60.6%; Pred. No. 4e-23;
Matches 57; Conservative 14; Mismatches 19; Indels
                                                          Score 499.5; DB 9;
Pred. No. 5.9e-44;
0; Mismatches 0;
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Pred. No. 2.4e-21;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 91
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Sequence 16, Application US/10090035
Patent No. US20020170089A1
GENERAL INFORMATION:
                                                      97.98;
98.98;
; ORGANISM: Triticum aestivum
US-10-090-035-18
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61.2%;
                                                                                       93; Conservative
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US-10-090-035-22
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; ORGANISM: Oryza sativa
US-10-090-035-16
                                                   Query Match
Best Local Similarity
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Best Local Similarity
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LENGTH: 91
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Best Local Similarity 33.3%;
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens
US-10-232-563-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                       GENERAL INFORMATION:
49 A---
                                                                                                 RESULT 13
US-09-888-615-64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MAYYQEVDYCSEEVRSVAP-AGFGRHGGGVQQHVVKEKFFEEVDTVSRAGANHHHHHGHHG 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/10232563;
Sequence 7, Application US/10232563;
Publication No. US20030087394A1
GENERAL INFORMATION:
APPLICANT: Sharma, Arun
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
CURRENT FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: US/10/232,563
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/316,453
PRIOR APPLICATION WINDER: US 60/316,453
SOFTWARE: FASESEO for Windows Version 4.0
SED ID NO 7
SED ID NO 7
FEWARD 1.00 7
                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: SImmons, Carl R.
TITLE OF INVENTION: Nucleal Acids Encoding Defense Inducible
TITLE OF INVENTION: Deteins and Uses Thereof
TITLE OF INVENTION: Proteins and Uses Thereof
FILE REFERENCE: 35718/242990
CURRENT APPLICATION NUMBER: US/10/090,035
CURRENT APPLICATION NUMBER: 002/28
PRIOR FILING DATE: 02/28/2001
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 80; DB 9; Length 359;
Pred. No. 1.4;
7; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 99;
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                       58 HG---GHGFYVRETRVEEDINTCTGEVHERRESFLARAN 93
                                                54 HGRGSGH-FEVRESKLEEDINTRTGEFHERKGNFSSKAD 91
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Pred. No. 5.4e-18;
9; Mismatches 22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: VARIANT
LOCATION: (1)...(99)
COTHER INFORMATION: Xaa = Any Amino Acid
US-10-090-035-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :(|||:||| ||| |||||| || NDYXMVRETKXEEDFNTCTGEFRER 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 GHGFVVRETRVEEDINTCTGEVHER 84
                                                                                                                                                                  Sequence 14, Application US/10090035 Patent No. US20020170089A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 15.7%;
Best Local Similarity 26.0%;
Matches 25; Conservative
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58.8%;
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Best Local Similarity 58.8
Matches 50; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 359
                                                                                                                                                    US-10-090-035-14
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21 GFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHHGHHG--GHG-----FVVRETRVEED 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 3353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/10232563
Sequence 2, Application US/10232563
Publication No. US20030087394A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: INSULIN RELATED TRANSCRIPTION FACTOR AND TITLE OF INVENTION: USSS THEREOF FILE REPERBNCE: 10276-072001
CURRENT FILING DATE: 2002-08-30
PRIOR PILING DATE: 2001-08-31
PRIOR FILING DATE: 2001-08-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.3%; Score 78; DB 9; Length 352; 29.9%; Pred. No. 2.1; tive 7; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48 GANHHHHHHHGHHGGH--GFVVRETRVEEDINTCTGEVHERRESFLA.90
175 ADDMGAGHHHGAHHTAHHHHSANHHHHHHHHGGSG 210
                                                                                                                                                                                                    APPLICANT: WHYTE, DAVID
APPLICANT: CARNEPEEL, SEAN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: WANNING, GERARD
APPLICANT: SUDARSANAM, SUCHA
TITLE OF INVENTION: NOVEL PROTEASES
FILE REFERENCE: 038602/1214
CURRENT APPLICATION NUMBER: US/09/888,615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 80;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 2001-06-26 PRIOR APPLICATION NUMBER: 60/214,047 PRIOR FILING DATE: 2000-06-26 NUMBER OF SEQ ID NOS: 150 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 64
                                                                                                               Sequence 64, Application US/0988615
Patent No. US20020064856A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KET: MOD_RES
LOCATION: (1891)
CTHER INFORMATION: Any amino acid
US-09-888-615-64
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230 QLVSMSVRELNRQLRGF 246

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| NESULT 15
| US-10-723-563-6
| Sequence 6, Application US/10232563
| Sequence 6, Application US/10232563
| Sequence 6, Application No. US200300873941
| GENERAL INFORMATION:
| APPLICANT: Sharms, Arun
| TITLE OF INVENTION: USES THEREOF
| FILE REPRENCE: 10276-02201-08-30
| CURRENT PILING DATE: 2001-08-31
| PRIOR FILLING DATE: 2001-08-31
| SEQ THOR FILLING DATE: 2001-08-31
| SEQ THOR FILLING DATE: 2001-08-30
| SEQ THO NOS: 22
| SOFTWARE: FastSO for Windows Version 4.0
| SEQ THO NOS: 22
| SEQ THO NOS: 23
| SEQ THO NOS: 23
| SEQ THO NOS: 23
| SEQ THO NOS: 24
| SEQ THO NOS: 25.08; Pred. No. 2.8; Pred. No. 2.
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Search completed: June 6, 2003, 13:02:10 Job time: 29 secs



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6, 2003, 12:49:03 ; Search time 18 Seconds
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152.018 Million cell updates/sec
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1 MAYYQEVDYCSEEVRSVAPA.....INTCTGEVHERRESFLARAN 93
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Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                 OM protein - protein search, using sw model
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Maximum.Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                      US-10-090-035-4
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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		ID	PCT-11592-06840-2	7 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	7-798-//0-90-50	05-09-252-571-2	US-09-434-065-2	US-08-789-275-4	US-08-789-275-5	115-09-086-010-2	118-08-272-146-20	118-00-070-079	02 03-019-029-9	0T-620-6/0-60-co	ņ	US-08-557-006C-43	US-08-072-064-1	US-08-072-064-4	110-073-064-6	0. 400 - 470 - 60 - 61	03-08-0/Z-064-8	PCT-0892-08558-1	US-08-448-418-97	US-09-079-029-11	US-09-184-658-40	US-09-461-474-17	US-09-126-980-2	115-09-476-482-2	7 707 71 70 70 70	9-609-716-60-60	05-09-423-439-44	8-80-	US-09-457-040B-36	
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US-08-974-549A-603 US-09-199-637A-201 US-09-199-637A-201 US-09-199-637A-199 US-09-199-637A-199 S US-08-927-394-2 US-08-927-394-2 US-08-911-769A-47 US-09-011-769A-64 US-09-011-769A-64 US-09-011-769A-64 US-08-101-769A-64 US-08-101-769A-69 US-08-101-769A-69 US-08-101-769A-69 US-08-101-769A-69 US-08-101-769A-69 US-08-101-769A-69 US-08-101-769A-69 US-08-101-769A-79 US-08-101-769A-79 US-08-101-769A-79 US-08-101-769A-79 US-08-101-769A-79 US-08-101-769A-79 US-08-101-769A-79	TRANSCRIPTION FACTOR AND METHODS TRANSCRIPTION FACTOR AND METHODS ATING SAME TING SAME The Americas - 7th Floor the Americas - 7th Floor TUS92/06840  1/US92/06840  5 07/746,485 31 31 31 31 32 32 32	re 79; DB 5; Length 414; d. No. 0.088; Mismatches 25; Indels
S00	PC/TUS92066  y ward homas homas homas to 10 10 10 10 10 10 10 10 10 10 10 10 10 1	Score Pred. 6; Miss
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133.2 133.2 133.1 122.9 122.9 122.6 122.6 122.6	111Con No.	15. Similarity 29. 1; Conservative
67.5 67.5 67.7 66.5 66.5 66.5 66.5 68.5 64.5 64.5 64.5	SEGUENCE 2, APPLICAT SEGUENCE 2, APPLICAT SEGUENCE 1, APPLICANT: SAPPLICANT: ON STREET: New YOT CONFORTS: NEW OPERATION NUM FILING DATE: 1 LANGE APPLICATION NUM FILING DATE: 1 LATORNEY/AGENT IN NAME: DEMINIS, NEGISTRATION NUM FILING DATE: 1 LELEPHONE: CALSATTON NUM FILING DATE: 1 LELEPHONE: CALSATTON NUM RETERENCE/AGENT IN NAME: DEMINIS, NAME: DEMINIS, NAME: CHARACTEE LENGTH: ALL AMINO ACT TOPOLOGY: 1 INGEMOLECULE TYPE: PARTICANTION CONTINGENT OF SECONDAL OF	Match Local Simes 21;
24444444444444444444444444444444444444	RESULT 1 PCT-US92-06 Sequence GENERAL APPLIC APPLIC APPLIC TITLE TITLE CONMUSS CONNES CONNUSS	Query M Best Lo Matches

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Sequence 2, Application US/09434065
; Sequence 2, Application US/09434065
; Patent No. 6107074
; GENERAL INFORMATION:
APPLICANT: SONG, HO Yeong
APPLICANT: ROTHE, Mike
TITLE OF INVENTION: TRAF2-Associated Kinase
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: 4 Embarcadero Center, 34th floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 763;
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Albritton & Herbert
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version #1.30
                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/252,571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 77; DB 2;
Pred. No. 0.33;
4; Mismatches
ADDRESSEE: Flehr, Hohbach, Test, Albritte
STREET: 4 Embarcadero Center, 34th floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                         NAME: Brezner, David J
REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: T96-005/A63613
TELECOMMUNICATION INFORMATION:
TELEBRONE: 415 781-1989
TELEFAX: 415 398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/434,06
                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/677,862
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 763 amino acids TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 15.1%;
Best Local Similarity 33.3%;
Matches 22; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: PatentI
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615 HHHHHG 620
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S
                                                                                                                                                                                                                                                                  FILING DATE
                                                                                                       94111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 4
US-09-434-065-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-252-571-2
                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
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            21 GFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHHGHHGGH-GFVVRETRVEEDINTCTG 79
                                     ---GGHGHAGHHHHHHHHPPMIALQPLVTDD----PT. 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14; Gaps
                                                                                                                                                                                                RESULT 2
US-08-677-862-2
| Sequence 2, Application US/08677862
| Sequence 2, Application US/08677862
| Patent No. 5874230
| GENERAL INFORMATION:
| APPLICANT: SOUG, HO YEONG
| APPLICANT: ROTHE, Mike
| TITLE OF INVENTION: TRAF2-Associated Kinase
| TITLE OF INVENTION: TRAF2-Associated Kinase
| TUNBER OF SEQUENCES: 2
| CORRESPONDENCES: 2
| CORRESPONDENCE ADDRESS: 3
| ADDRESSE: Flehr, Hobbach, Test, Albritton & Herbert
| STREET: 4 Embarcadero Center, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 77; DB 2; Length 763;
Pred. No. 0.33;
4; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/677,862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT IRRORANTON:
NAME: Brezner, David J
REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: 796-005/A63613
TELECOMUNICATION INFORMATION:
TELEPHONE: 415 781-1989
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 763 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09252571
Sequence 2, 581250
GENERAL INFORMATION:
APPLICANT: SONC, HO Yeong
APPLICANT: ROTHE, Mike
TITLE OF INVENTION: TRAF2-Associated Kinase
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   not relevant
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Best Local Similarity 33.3%;
Matches 22; Conservative
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96 QVHHHQEVILVQ 107
                                                           55 GGGDHGGG-----
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                                                                                                 80 EVHERRESFLAR 91
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---GANHHHHG 14; Gaps

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APPLICANT: Palleja, Estivill Xavier
APPLICANT: Palleja, Estivill Xavier
APPLICANT: Pritcherd, Melanie
APPLICANT: Vilato, Jordi Guimera
TITLE OF INVENTION: Human Gene Sequence of the Down Syndrome Critical
Fatent No. 635164
TITLE OF INVENTION: Region of Human Chromosome 21, Coding for A Serine-
TITLE OF INVENTION: Threonine Protein Kinase (MNB), Expressed in the
TITLE OF INVENTION: Nouronal Regions Affected in Down Syndrome
FILE REFERENCE: U 011114-4
CURRENT APPLICATION NUMBER: US/08/789,275A
NUMBER OF SEQ ID NOS: 6
SEQ ID NO 4
LENGTH: 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 SEEVRSVAPAGFGRHGG-----GVQQHVVKEKFEEVDTVSRA------GANHHHHG 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                            Query Match
15.1%; Score 77; DB 3; Length 763;
Best Local Similarity 33.3%; Pred. No. 0.33;
Matches 22; Conservative 4; Mismatches 26; Indels
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Pred. No. 0.33;
4; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        11 SEEVRSVAPAGFGRHGG-----GVQQHVVKEKFEEVDTVSRA----
                                                                                                         T96-005/A63613
APPLICATION NUMBER: 08/677,862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Brezner, David J
REGISTRATION NUMBER: 24,774
REFRENCE/DOCKET NUMBER: T96-TELECOMMUNICATION INFORMATION:
TELEPHONE: 415,781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/08789275A Patent No. 6251664 GENERAL INFORMATION:
                                                                                                                                                          TELEFAX: 415 398 3249
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 763 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 15.1%;
Best Local Similarity 33.3%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-434-065-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             615 ННИНЫ 620
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US-08-789-275-5
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11 SEEVRSVAPAGFGRHGG-----GVQQHVVKEKFEEVDTVSRA------GANHHHHG 56
APPLICANT: Palleja, Estivill Xavier
APPLICANT: Pritchard, Melanie
APPLICANT: Pritchard, Melanie
APPLICANT: Vilaro, Jordi Guimera
TITLE OF INVENTION: Human Gene Sequence of the Down Syndrome Critical
Patent No. 6251664
TITLE OF INVENTION: Region of Human Chromosome 21, Coding for A Serine-
TITLE OF INVENTION: Threonine Protein Kinase (MNB), Expressed in the
TITLE OF INVENTION: Neuronal Regions Affected in Down Syndrome
CURRENT APPLICATION NUMBER: US/08/789,275A
CURRENT FILING DATE: 1997-01-28
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
15.1%; Score 77; DB 4; Length 763;
Best Local Similarity 33.3%; Pred. No. 0.33;
Matches 22; Conservative 4; Mismatches 26; Indels
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Patent No. 6274338
GENERAL INFORMATION:
APPLICANT: GILINCHET, LAUTIE H. et al.
TITLE OF INVENTION: Human c-Maf Compositions and
TITLE OF INVENTION: Methods of Use Thereof
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: LAHIVE & COCKFIELD, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER:
FILING DATE: 2-FEB-1998
ATTORNEY/AGENT INPORMATION:
NAME: Kara, Catherine J.
REGISTATION NUMBER: 41,106
REFERENCE/DOCKET NUMBER: HUI-027CP
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: LAHIVE & COCKFIELD, LLP STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/086,010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (617)742-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 400 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Rat norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Massachusetts: USA
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      615 HHHHHG 620
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STATE: ME
COUNTRY:
                                                                                                                                                                                                                                                                                                   SEQ ID NO 5
LENGIH: 763
                                                                                                                                                                                                                                                                                                                                                                                                        ; FEATURE:
US-08-789-275-5
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Adams, Camilia W.

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APPLICANT
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                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Titmas, Richard C.
APPLICANT: Titmas, Richard C.
TITLE OF INVENTION: The Isolation and Production of
TITLE OF INVENTION: Catalytic Antibodies using Phage Technology
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: IGEN, Inc.
STREET: 1530 East Jefferson St.
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 11;
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Best Local Similarity 34.8%; Pred. No. 0.024;
Matches 16; Conservative 10; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32 HVVKEKFEEVDTVSRAGANHHHHHGHHGGHGFVVRETRV--EEDIN 75
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                         14.9%; Score 76; DB 4; Length 400; 31.6%; Pred. No. 0.2; tive 8; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER TEACHDLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 14-JUL-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSAQVQLQELE-IKRAAAHHHHHG---
                                                                                                                                                                                                                                    Sequence 39, Application US/08273146
Patent No. 5855885
GENERAL INFORMATION:
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; Patent No. 6342369
                                                                                                                                                                                                                                                                                              Smith, Rodger
McCafferty, John
Chiswell, David
Darsley, Michael J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Ryan, John W.
REGISTRATION NUMBER: 33,771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-984-8000
TELEFAX: 301-230-0158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 301-230-0158
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                     Fitzgerald, Kevin
Kenten, John H.
Martin, Mark T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 40 amino acids
                                 Query Match 14.99
Best Local Similarity 31.65
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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US-09-086-010-2
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GENERAL INFORMATION:

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256 EADYYCNSRDSS-----2NHVVFGGGTKL------TVLGAAAHHHHHG---- 293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 31; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.4%; Score 73.5; DB 4; Length 309; 32.9%; Pred. No. 0.29; tive 6; Mismatches 14; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPOTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPOTER: IBM PC compatible
COMPOTER: TEM PC COMPATING
SYSTEM: PC-DOS/MS-POS
                                                                                                                                                                                                                           ZIP: 94080
COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Adams, Camilia W.
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Chuntharapai, Anan
APPLICANT: Chuntharapai, Anan
APPLICANT: Kim, Kyung J.
TITLE OF INVENTION: Apo-2 Receptor
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STREET: California
COUNTRY: USA
ZIP: 94080
                                                                                                                                                                                                                                                                                                                                    SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,029
                                  TITLE OF INVENTION Apo-2 Receptor NUMBER OF SEQUENCES: 14 CORRESPONDENCE ADDRESS: ADDRESSEE Genentech, Inc. STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-079-029-10
; Sequence 10, Application US/09079029
Patent No. 6342369
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MATSCHANG, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1101
TELEPHONE: 650/255-5416
TELEPHONE: 650/255-5416
TELEPHONE: 650/255-5416
TELEPHONE: 650/952-9881
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
Chuntharapai, Anan
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294 ---AAEQKLISEEDLN 306
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                                                                                                                                      STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 14.49
Best Local Similarity 32.99
Matches 25; Conservative
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                        Kim, Kyung J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-079-029-9
                     APPLICANT:
  APPLICANT:
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GENERAL INFORMATION:
APPLICANT: Ber1, Rajindar K.
APPLICANT: Ber1, Rajindar K.
APPLICANT: Ber1, Rajindar K.
APPLICANT: Carling, David
APPLICANT: Forder, Robert A.
TITLE OF INVENTION: NUCLEIC ACID ENCODING AMP-ACTIVATED PROTEIN KINASE
FILE REFERENCE: NGAP/PHM37588/US7
CURRENT APPLICATION NUMBER: US/08/557,006C
PRIOR APPLICATION NUMBER: PCT/GB94/01093
PRIOR FILING DATE: 1994-05-20
PRIOR PAPLICATION NUMBER: GB 9318010.7
PRIOR RILING DATE: 1993-05-21
PRIOR FILING DATE: 1993-08-31
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 43
LENGTH: 633
                                                                                                                    17 VAPAGFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHHHHGHG---GHGFVVRET----
                                                   22; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                    Best Local Similarity 27.8%; Pred. No. 0.78;
Matches 20; Conservative 7; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 73; DB 4; Length 633;
Pred. No. 0.81;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08072064
Patent No. 6008046
GENERAL INFORMATION:
APPLICANT: FFRENCH-CONSTANT, RICHARD H.
APPLICANT: JACKSON, MEYER B.
TITLE OF INVENTION: DRUG AND PESTICIDE SCREENING
CORRESPONDENCE: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READALDE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: PETER G. CARROLL STREET: 220 Montgomery Street, Suite 2200 CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COCATION: (1)..(633)
CTHER INFORMATION: Yeast SNF1 polypeptide US-08-557-006C-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 United States of America
                                                                                                                                                                                                                                                                                                                     Sequence 43, Application US/08557006C Patent No. 6258547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.3%;
76.9%;
                                                                                                                           413 VGPGGPGGPGGGV----
                                                                                                                                                                                                     463 IGFSNIQQNVGT 474
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21 нннннннненся
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Best Local Similarity 76.9
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Yeast
                                                                                                                                                                                                                                                                      RESULT 12
US-08-557-006C-43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 26, Application US/08137614A
Patent No. 548796
GENERAL INFORMATION:
APPLICANT: Soderlund, David M.
APPLICANT: Knipple, Douglas C.
APPLICANT: Henderson, Joseph E.
TITLE OF INVENTION: Gene Encoding An Insect
TITLE OF INVENTION: Gamma-Aminobutyric Acid (GABA) Receptor Subunit
NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                                                                 DB 4; Length 312;
                                                                                                                                                                                                                                                                                                                                                                                                            14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                        Query Match 14.4%; Score 73.5; DB Best Local Similarity 32.9%; Pred. No. 0.29; Matches 25; Conservative 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           259 EADYYCNSRDSS-----GNHVVFGGGTKL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.3%; Score 73;
APPLICATION NUMBER: US/09/079,029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/137,614A FILING DATE: 15-OCT-1993
                                      CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAISCHANG, Diane L.
REGISTRATION NUMBER: 35,600
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/255-5416
TELEFAX: 650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Timian, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 1960
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716)263-1636
TELEFAX: (716)263-1600
                                                                                                                                                                                TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 312 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              297 ---AAEQKLISEEDLN 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 GFVVRETRV--EEDIN 75
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SEQUENCE CHARACTERISTICS:
LENGTH: 617 amino acids
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                                                                                                                                                                                                                                                        : 312 amino acids
Amino Acid
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ADDRESSEE: Nixon, Ha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-08-137-614A-26
                                                                                                                                                                                                                                                                                                   Linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14603
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                                                                                                                                                                                                                                                                                                                  US-09-079-029-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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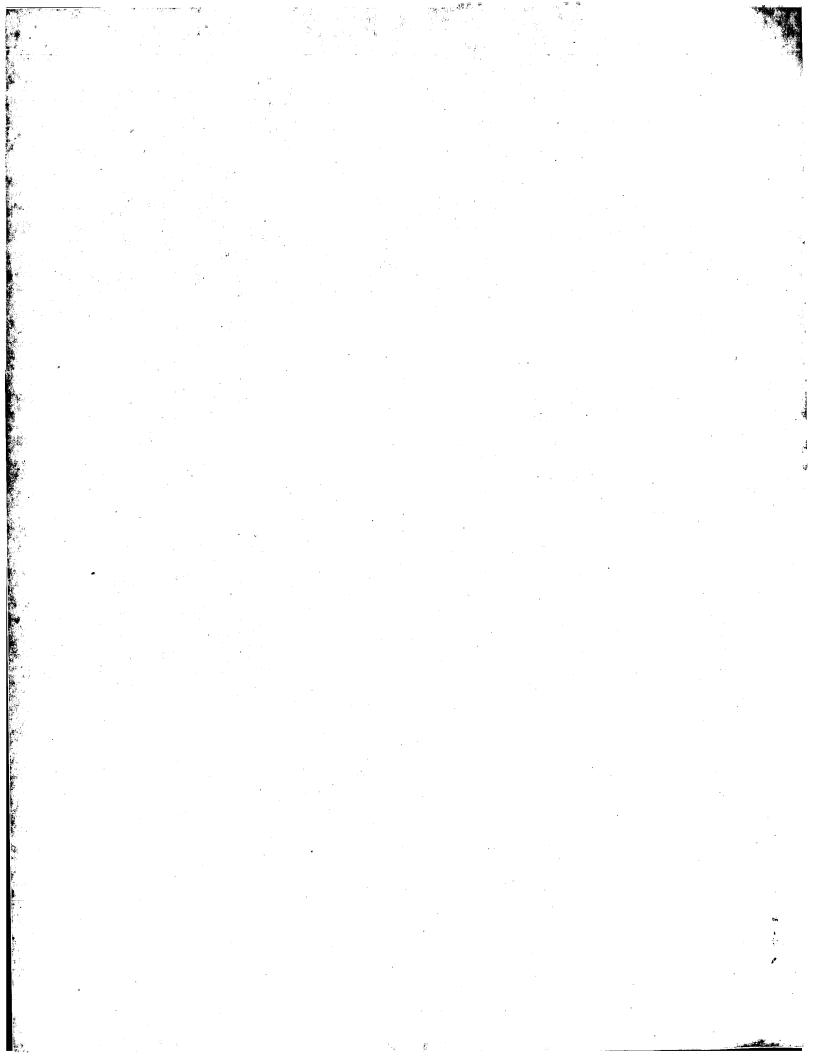
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17 VAPAGEGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHHGHG---GHGFVVRET---- 68
                                                                                                                                                                                                                                                                            17 VAPAGEGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHHGHHG---GHGFVVRET----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 637;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23; Indels
                                                                                                                                                                   DB 3; Length 637;
                                                                                                                                                                                                             23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: FFRENCH-CONSTANT, RICHARD H.
APPLICANT: JACKSON, MEYER B.
TITLE OF INVENTION: DRUG AND PESTICIDE SCREENING
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESS:
ADDRESSEE: PETER G. CARROLL
STREET: 220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMMUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 3;
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                                                                                                                                                                     14.3%; Score 73; DB 3; ilarity 27.8%; Pred. No. 0.81; Conservative 7; Mismatches
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United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/072,064
FILING DATE: 19930602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 19930602
CLASSIFICATION 435
CLASSIFICATION DATA:
APPLICATION NUMBER: US 770,881
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: 32,837
TELECOMMULTATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/08072064 Patent No. 6008046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 637 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           415/705-8410
                                                          : 637 amino acids
AMINO ACID
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                               434 VGPGGPGGPGGGV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide US-08-072-064-6
                                                                                                                                                                                                                                                                                                                                     69 ----RVEEDINT 76
TELEFAX: 415/397-8338
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                              TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            San Francisco
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Best Local Similarity
Matches 20; Conserve
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Best Local Similarity
Matches 20; Conservē
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ZIP: 94104
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US-08-072-064-6
                                                                                                                                      US-08-072-064-4
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STATE:
                                                            LENGIH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 73; DB 3; Length 637;
Pred. No. 0.81;
7; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/072,064
FILING DATE: 19930602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: FREENCH-CONSTANT, RICHARD H.
APPLICANT: JACKSON, MEYER B.
TITLE OF INVENTION: DRUG AND PESTICIDE SCREENING
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: PETER G. CARROLL
                                                                                                                                                                                                                                                                                                                                                                                                                                              CHROMOSOME/SEGMENT: III; polytene subregion 66F MAP POSITION: approximately map unit 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 220 Montgomery Street, Suite 2200 CITY: San Francisco STATE: California
                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 770,881
FILING DATE: 04-OCT-1991
ATTORNEY,AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
FEEFERNCE,DOCKET NUMBER: OPHD-00574
TELECOMMUNICATION INFORMATION:
TELECHNONE: 415,797-8338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPHD-00574
                                                                                                                                                                                                                                                                                                                                                                                             UNGARNISM: Drosophila melanogaster POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 19930602
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 04 - OCT-1991
ATTORNEY AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
          APPLICATION NUMBER: US/08/072,064
FILING DATE: 19930602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/08072064 Patent No. 6008046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: OF FELECOMMUNICATION INFORMATION: TELEPHONE: 415/705-8410
                                                                                                                                                                                                                                           TELEFAX: 415/39/-b330
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 637 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 27.8%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 434 VGPGGPGGPGGGV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    484 IGFSNIQONVGT 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 ----RVEEDINT 76
                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: unknown
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                   FILING DATE: 19
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94104
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US-08-072-064-4
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22; Gaps

69 ----RVEEDINT 76 ::::: | 484 IGFSNIQQNVGT 495 oy g

Search completed: June 6, 2003, 12:54:08 Job time: 19 secs



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Arabidopsis thalia
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Drosophila melanog
Drosophila melanog
ScFv 1b4 antibody
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## ALIGNMENTS

Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence. Arabidopsis thaliana protein fragment SEQ ID NO: 30923. AAG26460 ID AAG26460 standard; Protein; 441 AA. 990S-0121825. 990S-0123180. 990S-0123788. 990S-0125788. 990S-0126785. 990S-0127462. 990S-0127462. 990S-012834. 990S-012834. 2000EP-0301439 17-OCT-2000 (first entry) Arabidopsis thallana, EP1033405-A2 25-FEB-2000; 05-MAR-1999; 09-MAR-1999; 23-MAR-1999; 25-MAR-1999; 01-APR-1999; 06-APR-1999; 08-APR-1999; 16-APR-1999; 19-APR-1999; 06-SEP-2000 25-FEB-1999 AAG26460; RESULT 1 

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99US-0159329 99US-0159330

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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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9903-0160814. 9903-0160815. 9903-0160980. 9903-0160981. 9903-0160989. 47

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                                                      --HVVKEKFEEVDTVSRA-
                                             GANH-----HHHHGHHGGHGFVVRE----
                                                                                                                         ABB63257 standard; Protein; 168 AA
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32.9%;
   12 EEVRSVAPAGFGRHGGGVQQ-
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11-JUL-2000; 2000US-0614150.
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Matches 26; Conservative
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                                                                                                                                                                                                                                                     Drosophila melanogaster.
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N-PSDB; ABL07360.
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The sequence data for this patent did not form part of the printed The sequence data for this patent did not format directly from WIPO specification, but was obtained in electronic format directly from WIPO at frp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                   Gaps
                                                                                                                                                     8 DYCSEEVRSVAPAGFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHHGH---HGGH 61
                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                          Drosophila; developmental biology; cell signalling; insecticide;
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8
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                                                                                                           Length 488;
                                                                                                                                   18; Indels
                                                                                                                                                                                                                                                                                                     Drosophila melanogaster polypeptide SEQ ID NO 26127.
                                                                                                              DB 21;
                                                                                                                         0.073;
                                                                                                             16.5%; Score 84; DB 36.8%; Pred. No. 0.07 ive 10; Mismatches
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                                                                                                                                                                                                                                       ABB66445 standard; Protein; 1561 AA
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11-JUL-2000; 2000US-0614150.
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                                                                   99US-0161992.
99US-0161993.
99US-0162142.
              99US-0161406
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Best Local Similarity 23.9
Matches 28; Conservative
                                    99US-0161360
                                                           99US-016192(
                                              99US-016136
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N-PSDB; ABL10548.
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                                     26-OCT-1999;
26-OCT-1999;
28-OCT-1999;
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29-OCT-1999
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Matches
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ABB66445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
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                                                              Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 16563; 21pp + Sequence Listing; English.
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Drosophila melanogaster polypeptide SEQ ID NO 16563
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Pred. No. 0.025
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Myers EW;
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us-10-090-035-4.rag

27-FEB-2002

AAG66039;

RESULT 6

15-NOV-2001.

Synthetic.

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 GFGRHGGGVQQHVVKEKFEEVDTVSRAGANHH-------HHHGHHGGHGFVVRETR 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL5737-ABB72072).
                                                                                                              Drosophila; developmental biology; cell signalling; insecticide;
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                                                                           Drosophila melanogaster polypeptide SEQ ID NO 29814.
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Pred. No. 0.13;
9; Mismatches 38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Myers EW;
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11-JUL-2000; 2000US-0614150.
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Best Local Similarity 26.6%;
Matches 21; Conservative
                                         (first entry)
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                                                                                                                                                                           Drosophila melanogaster.
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                                                                                                                                         pharmaceutical
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  ABB67674;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  encoding the protein and expressing the protein in vivo. (I) is used as an immunogen to produce an antibody against it. The antibodies are useful for modulating angiogenesis at a site. Polynucleotides encoding (I) is useful in gene therapy technique for treating above mentioned medical conditions. The present sequence represents the scFv lb4 antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to modulating anglogenesis at a site by supplying a composition comprising a variant Ryk protein (I) (a member of the receptor tyrosine kinase family), or modulating formation of calls into capillary like structures by contacting the calls with a composition comprising (I). The method is useful modulating anglogenesis at a site (endothelia) within a human) or modulating the formation of calls (I) is useful for preventing, treating or ameliorating a medical degeneration, cardiovascular disease, wound, pregnancy, or a clinical degeneration, cardiovascular disease, wound, pregnancy, or a clinical condition involving anglogenesis in the reproductive system, including protein is supplied to the individual as a source of polynocleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modulating anglogenesis at a site, for treating or preventing cancer, metastasis, diabetic retinopathy, cardiovascular disease, wound by supplying composition comprising variant Ryk protein to the site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 271;
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Pred. No. 0.071;
9; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Mismatches
                                 AAG66039 standard; Protein; 271 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Examples; Page 79-80; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB67674 standard; Protein; 347 AA,
                                                                                                                                                                                                                                                                                                                                                                                        09-MAY-2001; 2001WO-US15043.
                                                                                                                                                                                                                                                                                                                                                                                                                           10-MAY-2000; 2000US-0568783.
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Best Local Similarity 34.0
Matches 17; Conservative
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N-PSDB; AAI67770.
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Sequence

225

ò 윱 RESULT 7 ABB67674 ID ABB6

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AX Arabidopsis thaliana.

XX Arabidopsis thaliana.

XX 06 - SEP - 2000.

XX 16 - SEP - 2000.
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990S-0145085. 990S-0145087. 990S-0145192. 990S-0145195. 990S-0145145. 990S-014524. 990S-014524. 990S-014524. 990S-0145918.

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25-MAR-1999;
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01-APR-1999;
08-APR-1999;
16-APR-1999;
16-APR-1999;
23-APR-1999;
23-APR-1999;
23-APR-1999;
28-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 SEEVRSVAPAGFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHHHHHGHGGHG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                      13.8%; Score 80.5; DB 21; Length 384; Conservative 4; Mismatches 28; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana protein fragment SEQ ID NO: 13564.
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99US-0161920
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25-0CT-1999;
25-0CT-1999;
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Matches 19;
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99US-0142920

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99US-0144332

99US-0144331

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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                                                                                                                                                                                                                                                                                                         Length 388;
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22-SEP-1999; 23-SEP-1999; 24-SEP-1999;

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Gaps

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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                                                                                                                                                                                                           Score 80.5; DB 21; Length 388; pred. No. 0.15; 4; Mismatches 28; Indels 1
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Best Local Similarity 36.5%;
Matches 19; Conservative
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19-APR-1999;
21-APR-1999;
  12-OCT-1999)
13-OCT-1999)
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26-OCT-1999;
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09-MAR-1999
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25-MAR-1999
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2-OCT-1999;
5-OCT-1999;
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                                                                                                                                                                                                                                                               RESULT 11
AAG13901
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RR 20.-10.1999 9918-0146622
RR 21.-01.1999 9918-0146624
RR 21.-01.1999 9918-0146624
RR 21.-01.1999 9918-0146626
RR 22.-01.1999 9918-0146668
RR 22.-01.1999 9918-0146068
RR 22.-01.1999 9918-0140687
RR 22.-01.1999 9918-0140687
RR 22.-01.1999 9918-0140687
RR 22.-01.1999 9918-0140224
RR 22.-01.1999 9918-014024
RR 23.-01.1999 99
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                             1; Gaps
                                                                                                                                                                                                                                                        290 SNGVREMYRCG-GIFGGFMINTSSSSSSSSSWVSSSAEHHHHHNHNMGHG 340
                                                                                                                                                                                                                                           11 SEEVRSVAPAGFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHGHHGGHG
                                                                                                                                                                                                             Length 396;
                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana protein fragment SEQ ID NO: 62933.
                                                                                                                                                                                                                            28;
                                                                                                                                                                                                          / Match 15.8%; Score 80.5; DB 21;
Local Similarity 36.5%; Pred. No. 0.15;
Los 19; Conservative 4; Mismatches 28;
                                                                                                                                                                                                                                                                                                       AAG49724 standard; Protein; 396 AA.
990S-0159637.
990S-0159534.
990S-0160741.
990S-0160767.
990S-0160776.
990S-0160814.
990S-0160980.
990S-0160980.
990S-0161405.
990S-0161350.
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99US-0123548.
99US-0125788.
99US-0125788.
99US-01267465.
99US-0127465.
99US-0128714.
99US-0128714.
99US-013077.
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99US-013077.
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99US-013074.
99US-013074.
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14-0CT-1999;
14-0CT-1999;
21-0CT-1999;
21-0CT-1999;
21-0CT-1999;
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05-MAR-1999;
03-MAR-1999;
23-MAR-1999;
29-MAR-1999;
01-APR-1999;
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16-APR-1999;
16-APR-1999;
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23-APR-1999;
23-APR-1999;
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05-MAY-1999;
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Best Local S1
Matches 19;
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PR 06-NAY-1999; 99US-0132486.
PR 17-NAY-1999; 99US-0133418.
PR 14-NAY-1999; 99US-0133421.
PR 14-NAY-1999; 99US-013352.
PR 16-JUN-1999; 99US-013352.
PR 16-JUN-1999; 99US-013345.
PR 16-JUN-1999; 99US-013945.
PR 18-JUN-1999; 99US-013945.
PR 13-JUN-1999; 99US-014335.
PR 13-JUN-1999; 99US-014335.
PR 13-JUN-1999; 99US-014335.
PR 13-JUN-1999; 99US-014433.
PR 23-JUN-1999; 99US-014433.
PR 23
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Second	99US-0147204. 99US-0147204. 99US-0147192. 99US-0147260. 99US-0147303. 99US-0147493. 99US-014819. 99US-0148341. 99US-0148341. 99US-0148341. 99US-0148341. 99US-0148341. 99US-0148341. 99US-0149368. 99US-0149722. 99US-0149722. 99US-0149929.	US-015106 US-015106 US-015108 US-015143 US-015143 US-015375 US-015473 US-015473 US-01565 US-01565 US-015715 US-015715 US-015715 US-015715 US-015715 US-015715 US-015715 US-015715 US-015715 US-015715 US-015715 US-015715 US-015715 US-015715	100 - 015802 100 - 015802 101 - 015829 102 - 015829 103 - 015923 103 - 015933 104 - 015933 105 - 015963 107 - 015963 108 - 015963 108 - 015963 108 - 015963 108 - 015963 108 - 015963 108 - 016074
JUL-1999	04-AuG-1999; 05-AuG-1999; 05-AuG-1999; 06-AuG-1999; 06-AuG-1999; 09-AuG-1999; 10-AuG-1999; 11-AuG-1999; 11-AuG-1999; 11-AuG-1999; 11-AuG-1999; 11-AuG-1999; 11-AuG-1999; 12-AuG-1999; 20-AuG-1999; 21-AuG-1999; 21-AuG-1999; 21-AuG-1999; 21-AuG-1999; 21-AuG-1999; 21-AuG-1999; 21-AuG-1999; 21-AuG-1999; 21-AuG-1999; 21-AuG-1999; 21-AuG-1999;	- ANG - 1999 - ANG - 1999 - ANG - 1999 - SEP	7-0CT-199 2-0CT-199 2-0CT-199 3-0CT-199 3-0CT-199 4-0CT-199 4-0CT-199 4-0CT-199 1-0CT-199 1-0CT-199
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990S-0134370.
990S-0134768.
990S-01351241.
990S-0135124.
990S-0135629.
990S-0137528.
990S-0137528.
990S-0137528.
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990S-013452.
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990S-0139455.
990S-0139459.
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990S-0139460.
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990S-0142977
990S-0143624
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9905-0144331
9905-0144332
9905-0144334
9905-0144334
9905-0144355
9905-0144884
9905-0144884
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9905-0145085
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99US-0145913
             14 - MAY - 1999;

18 - MAX - 1999;

20 - MAX - 1999;

21 - MAY - 1999;

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30-JUN-19
01-JUL-19
             1;
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                                                                                                                                                                                                                                                    11 SEEVRSVAPAGFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHHHHHHGHHGGHG 62
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15.8%; Score 80.5; DB 21;
Best Local Similarity 36.5%; Pred. No. 0.15;
Matches 19; Conservative 4; Mismatches 28;
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  990S-0160814.
990S-0160815.
990S-0160980.
990S-0160989.
990S-0161404.
990S-0161405.
990S-0161359.
990S-0161359.
990S-0161359.
990S-0161360.
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990S-0123788
99US-0125788
99US-0126264
99US-0126264
99US-0126264
99US-0128234
99US-0128146
99US-0130891
99US-0130891
99US-0130891
99US-0131863
99US-0132486
99US-0132486
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21-0CT-1999;
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22-0CT-1999;
25-0CT-1999;
25-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
28-0CT-1999;
28-0CT-1999;
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28-APR-1999;
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05-MAY-1999;
06-MAY-1999;
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AAG49723
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99US-0155139.
99US-0155486.
99US-0155659.
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99US-0154039.
99US-0154779.
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990S-0148565.
990S-0148684.
990S-0149368.
990S-0149175.
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99US-0149723.
99US-0149929.
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99US-0149930.
99US-0150566.
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99US-0151438
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99US-0153758
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                                                                           99US-0147493
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25-OCT-1999;
25-OCT-1999;
                            02-AUG-1999;
03-AUG-1999;
04-AUG-1999;
04-AUG-1999;
05-AUG-1999;
05-AUG-1999;
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06-AUG-1999;
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                                                                                                   12-AUG-1999
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21-OCT-19
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27-AUG-19
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The present invention relates to the isolation of novel human proteases, and the nucleic acids encoding them. The sequences of the invention are useful for treating diseases and disorders such as cancers (e.g. breast, colon, lung), immune-related diseases and disorders (e.g. inflammatory diseases and asthma), cardiovascular diseases (e.g. restenosis and coronary thrombosis), brain or neuronal-associated diseases, metabolic disorders (e.g. diabetes, obesity), inflammatory disorders (e.g. rheumatorid arthritis and psoriasis), central or peripheral nervous system diseases, migraines, pain, sexual dysfunction, hypertension, psychotic disorders, neurological disorders, hypotension, hypertension, psychotic disorders, neurological disorders (e.g. Alzheimer's disease, Parkinson's disease) and dyskinesias.

The nucleic acids and polypeptides are also useful for treating viral
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; protease; cancer; immune-related disorder; cardiovascular disease; neuronal-associated disease; metabolic disorder; inflammatory disorder; nervous system disorder; sexual dysfunction; pain; mood disorder; hypertension; psychotic disorder; neurological disorder; dyskinesia; viral infection; human immunodeficiency virus; HIV; non-viral infection; ocular disease; cytostatic; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding novel human proteases, useful for useful treating diseases and disorders such as cancers, immune-related diseases and disorders, cardiovascular disease (e.g. restenosis) and inflammatory disorders
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                                                                                                                                                                        1;
                                                                                                                                                                                                   11 SEEVRSVAPAGFGRHGGGVQQHVVKEKFEEVDTVSRAGANHHHHHHHHGHHGGHG
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                                                                                                                                      Length 405;
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                                                                                                                                                                        Indels
                                                                                                                                                                        28;
                                                                                                                                           DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                  Amino acid sequence of novel human protease #5.
                                                                                                                                          Score 80.5; DB Pred. No. 0.16; 4; Mismatches
                                                                                                                                                                                                                                                                                                                      AAU82706 standard; Protein; 3353 AA.
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                                                                                                                                             15.8%;
               99US-0161359.
99US-0161360.
99US-0161361.
99US-0161920.
99US-0161993.
99US-0161993.
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 39US-0161406
                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-139913/18.
N-PSDB; ABK31748.
                                                                                                                                          Query Match
Best Local Similarity
Matches 19; Conserva
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25-OCT-1999;
26-OCT-1999;
26-OCT-1999;
                                                                          28-0CT-1999;
28-0CT-1999;
29-0CT-1999;
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                                                 26-0CT-1999
                                                                28-OCT-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes a novel multimeric cytomegalovirus (CMV) antigen
infections caused by human immunodeficiency virus (HIV), and non-viral infections such as ocular disease (e.g. glaucoma) and macular degeneration. AAU82702-AAU82760 represent the novel human proteases of the invention.
                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Multimeric cytomegalovirus antigen useful as an immunoassay reagent, and which comprises at least two p52 peptide sequences
                                                                                                                                                                                                                                                                                                                                               CMV-p52 antigen; multimeric; immunoassay; IgM; immunoglobulin M; diagnosis; infection; reactivation.
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                                                                                            Score 80; DB 23; Length 3353;
Pred. No. 2.7;
9; Mismatches 19; Indels
                                                                                                                                                              48 GANHHHHHHGHHGGH--GFVVRETRVEEDINTCTGEVHERRESFLA 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 79; DB 22; Length 87;
Pred. No. 0.035;
5: Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                    Human cytomegalovirus dimeric p52 antigen protein.
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                                                                                                                                                                                                                                       AAB11465 standard; Protein; 87 AA.
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                                                                                            15.7%;
33.3%;
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32.1%;
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                                                                                        Query Match
Best Local Similarity 33.33
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 15.5
Best Local Similarity 32.1
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                        Human cytomegalovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-041727/06.
N-PSDB; AAC81969.
                                                                 3353 AA;
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                                                                 Seguence
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Search completed: June 6, 2003, 12:50:08 Job time: 32.5 secs

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Sequence 1, Appli
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                                                                June 16, 2003, 01:55:01; Search time 40.4096 Seconds (without alignments) 4356.204 Million cell updates/sec
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                                                                                                                 Description
                                                                                                                                                                                                                                                                                                                                   Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodatu/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodatu/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodatu/1/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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1 US-08-103-840A-1

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1 US-08-476-519-11

1 US-08-440-856A-9

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1 US-08-133-711-44

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1 US-08-133-711-44

1 US-08-13-711-42

1 US-08-13-125-11

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1 US-08-13-125-11

1 US-08-17-501-23

1 US-08-479-382-23

1 US-08-479-382-23
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                                                                                                                                                                                                  441362 seqs, 153338381 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-197-649-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                         OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                 IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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4411529 4
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Match Length DB
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1187 1
1936 4
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Perfect score:
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No.
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Sequence 23, Appl. Sequence 3, Appl. Sequence 19, Appl. Sequence 11, Appl. Sequence 5, Appl. Sequence 5, Appl. Sequence 5, Appl. Sequence 5, Appl. Sequence 16, Appl. Sequence 17, Appl. Sequence 17, Appl. Sequence 18, Appl. Sequence 18, Appl. Sequence 18, Appl. Sequence 19, Appl. Sequence 19, Appl. Sequence 19, Appl.	ition by Reverse Translation	Length 390; Indels 0; Gaos 0;	16			
1485 4 US-09-195-716-23 1520 4 US-09-105-537-32 36708 4 US-09-105-537-5 38506 3 US-09-105-537-5 28506 3 US-09-105-537-5 13853 5 PCT-US92-06840-1 1777 1 US-08-173-508-5 1777 2 US-08-251-310-5 1777 3 US-08-251-310-5 1777 3 US-08-251-7-5 13842 4 US-09-105-537-30 1845 4 US-09-105-537-30 291 3 US-08-110-6468-16 291 3 US-08-110-6468-16 1258 2 US-08-31-818-16 1258 2 US-08-31-818-16 1258 4 US-08-31-818-16 1265 4 US-08-31-818-16 1496 4 US-08-765-907A-7	ALIGNMENTS  9  1ypeptide Evolu  1197,649  9,461  9,055  1,968  1,968  Artificial Seepeat of ACG f  ing NCOI restri	10.9%; Score 62.6; DB 4; 52.0%; Pred. No. 0.0014; vative 0; Mismatches 129;		GCCGCCACGGCGCGCGCTCCAGCACCTCGTCAAGGAGAAGTTCGAGGAGGTCGACA 	CGGTCTCACGCCGGCGCGAACCACCACCACCACCATGGTCACCACGGCGGCCACGGCT 	TCGTGGTGCGCAGACCAGGGTCGAAGAGACATCAACACCTGCACCGGGGAGGTCCACG 11
28 46 80 30 45.8 8.0 33 45.8 8.0 33 44.4 7.7 7.7 36 44.4 7.7 7.7 7.7 7.7 7.8 7.9 7.9 7.9 7.9 7.9 7.9 7.9 7.9	SULT 1 Sequence 7, Application US/0919764 Sequence 7, Application US/0919764 Sequence 7, Application US/0919764 Sequence 7, Application US/0919764 Setent No. 619450  APPLICANT: Gld, Larry APPLICANT: Tuerk, Craig APPLICANT: HEXO, Jonathan D. FILE REFERENCE: WEXO, ZC1-CON CURRENT FILING DATE: 1998-11-23 EARLIER APPLICATION NUMBER: 07/738 EARLIER FILING DATE: 1991-08-01 EARLIER FILING DATE: 1990-08-02 SOFTWARE: PATENTING DATE: 1990-08-02 SOFTWARE: ARTIFICIAL SEQUENCE FEATURE: OTHER INFORMATION: Description of OTHER INFORMATION: fragments havi-	Query Match Best Local Similarity 52 Matches 140; Conservativ	103 ACTACCAGG          109 ACGACGACG	. 163 GCGCCACG 	223 CGGICICAC   1 229 ACGACGACG	283 TCGTGGTGC       289 ACGACG
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; OTHER INFORMATION: H37Rv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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STATE: Missouri
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US-08-476-519-10
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                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE: OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-22007, 00
CURRENT APPLICATION NUMBER: US/09/103, 840A
CURRENT FILING DAILE: 1998-06-24
                                                                                                                                                                                                         APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-22007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
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Pred. No. 0.028;
0; Mismatches 98; Indels
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                           343 AGCGCAGGGAGAGCTTCCTCGCCAGGGCT 371
                                             TYPE: DNA ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Mycobacterium tuberculosis
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                                                                                                                                        Sequence 2, Application US/09103840A
Patent No. 6294328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 53.3%;
Matches 112; Conservative
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LENGTH: 4411529
                                                                                                                            JS-09-103-840A-2/c
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                                                                                            149 CCCGGCCGGCTTCGGCCGCCGCCGCGGCGTCCAGCAGCACGTCGTCAAGGAAGTT
                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Barry, Gerard F.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Krohn, Bradley M.
TITLE OF INVENTION: No. 5750876el Isoamylase Gene, Compositions
TITLE OF INVENTION: Containing It and Methods of Using Isoamylases
NUMBER OF SEQUENCES: 11
  Length 4411529;
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Score 53.2; DB 4; Length 4 Pred. No. 0.028; 0; Mismatches 88; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Grace L. Bonner, Monsanto Company, BB4F
STREET: 700 Chesterfield Parkway No. 5750876th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,519
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/281902
FILING DATE: 28-UL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bonner, Grace L.
NAME: Bonner, Grace L.
REGISTRATION NUMBER: 32,963
REFERENCE/DOCKET NUMBER: 38-21(13577)A
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10, Application US/08476519
Patent No. 5750876
                                                                                                                                                                                                                                                                                                                                                                                                                                               3932908 ceeceeceece 3932921
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TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
          Query Match 9.3%;
Best Local Similarity 54.6%;
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                CGGCGAGGTCCACG 342
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nucleic acid
EDNESS: double
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Sequence 1, Application US/08476519; Patent No. 5750876; General Information: Thromation: Thromation: APPLICANT: Rishore, Ganesh M.; APPLICANT: Kishore, Ganesh M.; APPLICANT: Kishore, Ganesh M.; APPLICANT: Krohn, Bradley M.; TITLE OF INVENTION: No. 5750876el Isoamylase Gene, Compositions TITLE OF INVENTION: Containing It and Methods of Using Isoamylases; NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS: ADDRESSE: Grace L. Bonner, Monsanto Company, BB4F
STREET: 700 Chesterfield Parkway No. 5750876th
CITY: St. Louis
STRIET: Missouri
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 51.8; DB 1; Pred. No. 0.025; 0; Mismatches 87;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/281902
FILING DATE: 28-JUL-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application PC/TUS9509323
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Bonner, Grace L.
REGISTRATION NUMBER: 32,963
REFERENCE/DOCKET NUMBER: 38
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-7286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (314)537-7286
TELEFAX: (314)537-76647
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 234 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 54.5%;
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1150 GCGCGGTCGAC 2160
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                           US-08-476-519-1
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                                                     Gaps
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TITLE OF INVENTION: Containing It and Methods of Using Isoamylases
NUMBER OF SEQUENCES: 11
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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9.0%; Score 51.8; DB 1; Length 2244;
54.5%; Pred. No. 0.025;
Live 0; Mismatches 87; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 9.0%; Score 51.8; DB 5; Length 2244; Best Local Similarity 54.5%; Pred. No. 0.025; Matches 104; Conservative 0; Mismatches 87; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US95/09323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/281902
FILING DATE: 28-JUL-1994
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10, Application PC/TUS9509323 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 2244 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                   Best Local Similarity 54.5
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                               2057 GCGCGGTCGAC 2067
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY: CDS
; LOCATION: 1...2
PCT-US95-09323-10
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  Query Match
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STREET: 2000 PENNSYLVANIA AVE. N.W. CITY: WASHINGTON
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (202) 887-15:
(202) 887-0763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1288 base pairs
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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EDNESS: both
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US-08-440-856A-9
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Best Local Similarity
Matches 112; Conserva
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STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: FLEISCHAAN, Robert D.
APPLICANT: FLEISCHAAN, Robert D.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: PRASER, John C.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PAGENTIN Ver. 2.1
SEQ ID NO 1
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                Novel Isoamylase Gene, Compositions
Containing It and Methods of Using Isoamylases
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ilarity 52.6%; Pred. No. 0.078;
Conservative 0; Mismatches 100; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2334;
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Pred. No. 0.025;
0; Mismatches 87; Indels
                    TITLE OF INVENTION: Novel Isoamylase Gene, Compositions TITLE OF INVENTION: Containing it and Methods of Using NUMBER OF SEQUENCES: 11
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Mycobacterium tuberculosis OTHER INFORMATION: H37Rv
                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/281902
FILING DATE: 28-JUL-1994
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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Patent No. 6294328
                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 54.5%;
Matches 104; Conservative
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STRANDEDNESS: doub
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Matches 111; Conserv
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                                                                                                                                                                                                FILING DATE:
CLASSIFICATION:
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3749067 GAGCTGCGGCACCTGAATCGTCAACCTCGGCAACGTCGGCAGCTACAAC 3749008
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                                                                                       Gaps
                                                        192 GTCGTCAAGGAGAAGTTCGAGGAGGTCGACACGGTCTCACGCGCCGGCGCCAACCACCAC
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                                                                                                                                                                                                                                                                                                                                                          18-08-440-856A-9
Sequence 9, Application US/08440856A
Sequence 9, Application US/08440856A
Sequence 9, Application US/08440856A
Sequence 9, Application US/08440856A
SEQUENCE OF INVENTION: MATERIALS AND METHODS FOR PRODUCING TITLE OF INVENTION: PLANTS WITH SINGLE-SEX FLOWERS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/440,856A FILING DATE: 15-MAY-1995 CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.7%; Score 50.2; DB 1;
ilarity 43.9%; Pred. No. 0.05;
Conservative 20; Mismatches 123;
                                                                                                                                                                                                                                                        312 GACATCAACACCTGCACCGGCGAGGTCCACG 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: MILLMAN, ROBERT A.
REGISTRATION NUMBER: 36,217
REFERENCE-DOCKET NUMBER: 05463-20001.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1517
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us-10-090-035-3\_1.rni

; FEATURE: . CDS ; NAME/KEY: CDS ; LOSTION: 49455100 : FEATURE.	KEY: ION:	; LOCATION: 62946680 ; FEATURE: ; NAME/KEY: ; LOCATION: 67897079	FEATURE:  NAME/KEY: exon  LOCATION: 2153.2332	; NAME/KEY: exon ; LOATION: 24372832 ; FEATURE:	NAME/KEY: exon LOCATION: 29443027	NAME/KEY: exon LOCATION: 3900.4121	NAME/KEY: exon LOCATION: 44924596	NAME/KEY: exon LOGATION: 47234812	; FALURE: exon; COCATION: 4945.5100	exon		; NAME/KEY: exon ; LOCATION: 62946680 : FEATURE	NAME/KEY: exon ; LOCATION: 67897079	; realons: ; hamb/KEx: intron ; LOCATION: 21542331		FEATURE:		; NAME/KEY: intron ; LOCATION: 3901.4120	NAME/KEY: intron	; FATURE: intron : NAME/KEY: 1ntron : LOCATION: 47244811	FALUKE: Intron DOCATION: 49465099	NAME/KEY: intron LOCATION: 51996195	; NAME/KE: intron ; LOCATION: 6295.6679 ; FPRAMIDE:	NAME/KEY: intron ; LOCATION: 67907078 ; FEATURE:
296 GACCAGGGTCGAAGAGACATCAACACCTGGACGGGGAGGTCCACGAGGGAGAG 355 	356 CTTCCTCGCCAGGC 370 	SULT 10 -08-250-848-2 Sequence 2, Application US/08250848	Patent No. 5856177 GENERAL INFORMATION: APPLICANT: Hudspeth, Richard L.	TITLE OF INVENTION: PROMOTERS DERIVED FROM THE MAIZE TITLE OF INVENTION: PHOSPHOENOLPKRUVATE CARBOXYLASE GENE INVOLVED IN C4	NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS: ADDRESSES	ADORGESTE CHITETE, Parker 6 Hale STREET: P.O. Box 7068 CITY: Pasadena	COUNTRY: USA COUNTRY: USA COUNTRY: USA COUNTRY: USA	CONTROL TYPE: Floppy disk COMPUTER: Floppy disk COMPATER: IBM PC COMpatible	OPENATING SISTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:	APPLICATION NUMBER: US/08/250,848 FILING DATE:	CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:	NAME: Sharp Esq., Janice A. REGISTRATION UNMERS: 34,051	TELECOMMUNICATION INFORMATION: TELECOMMUNICATION: 0.1010; 795-5643	INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERS.	LENGTH: 7559 base pairs TYPE: nucleic acid	double	NOTICE TIPE: UNA (genomic) ANTO-TETICAL: NO ANTO-TETICAL: NO	Ë	NAME/KEY: CDS LOCATION: 2153.2332	FANDEKE: NAME/KE: LOCATION: 2437.2832	FANDEKE: NAME/KE: LOCATION: 2944.3027	NAME/KEY: CDS LOCATION: 39004121	FEMIORE: NAME/KEY: CDS LOCATION: 4492.,4596	NAME/KEY: CDS LOCATION: 47234812

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296 GACCAGGGICGAAGAGGACAICAACACCIGCACGGGGGGGICCACGAGGGGAGAG 355
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Patent No. 525463
GENERAL INFORMATION:
APPLICANT: 2019, Werner
TITLE OF INVENTION: Methods and reagents for detection of
TITLE OF INVENTION: pathogens using superoxide dismutase gene
TITLE OF INVENTION: targeting
NUMBER OF SOURNES: 44
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                            Length 1236;
                                                                                                                                                                             8.5%; Score 48.6; DB 1; Length 1
49.4%; Pred. No. 0.1;
tive 0; Mismatches 129; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STRATE: NU
COUNTRY: U.S.A.
ZIP: 07110-1199
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPUTER: Date Compatible
OMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/133,711
ATTINC NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EP 92810780.4
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APPLICATION NUMBER: EP 928107
FILING DATE: 13-0CT-1992
ATTOREY/AGENT INFORMATION:
NAME: Patricla S. Rocha
REGISTATION NUMBER: 31,054
REFERENCE/DOCKET NUMBER: 4095,
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (201) 235 5000 TELEFAX: (201) 235 3500 INFORMATION FOR SEQ ID NO: 44: SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 1236 base pairs TYPE: nucleic acid STRANDEDNESS: sinal TOPOLOGY
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Best Local Similarity 49.4
Matches 126; Conservative
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CLASSIFICATION: 435
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US-08-440-856A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: DELLAPORTA, STEPHEN L.
TITLE OF INVENTION: MATERIALS AND METHODS FOR PRODUCING
TITLE OF INVENTION: PLANTS WITH SINGLE-SEX FLOWERS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 15-MAY-1995
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: MILLMAN, ROBERT A.
REGISTRATION NUMBER: 36,217
REFERENCE/DOCKET NUMBER: 05463-20001.00
TELECOMMUNICATION INFORMATION:
TELECHONE: (202) 887-1517
TELEFAX: (202) 887-0763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVE. N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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MEDIUM TYPE: Floppy
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2153..7079
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7314..7319
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NAME/KEY:
FEATURE:
NAME/KEY:
LOCATION:
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LOCATION:
FEATURE:
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US-08-250-848-2
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                                       NAME/KEY:
                                                         LOCATION:
FEATURE:
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Pred. No. 0.13:
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                                                                                                                                                   0; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: DELLAPORTA, STEPHEN L.
TITLE OF INVENTION: MATERIALS AND METHODS FOR PRODUCING
TITLE OF INVENTION: PLANTS WITH SINGLE-SEX FLOWERS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match

8.4%; Score 48; DB 1; Length 118
Best Local Similarity 47.6%; Pred. No. 0.14;
Matches 141; Conservative 0; Mismatches 155; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION NUMBER: US/08/440,856A
FILING DATE: 15-MAY-1995
CLASSIFICATION: 800
                                    MOLECULE TYPE: CDNA
) ORIGINAL SOURCE:
) ORGANISM: Actinomyces viscosus/SOD gene
US-08-133-711-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 2000 PENNSYLVANIA AVE. N.W. CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08440856A Patent No. 5750873 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: MILLMAN, ROBERT A.
REGISTRATION NUMBER: 36,217
REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
                                                                                                                  Query Match
Best Local Similarity 50.9%;
Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFHONE: (202) 887-1517
TELEFAX: (202) 887-0763
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nucleic acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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US-08-440-856A-2
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COTHER INFORMATION: CDC 1551
COTHER INFORMATION: "n" bases at various positions throughout the sequence
COTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
                                                                                                                         199 AGGAGAAGTTCGAGGAGGTCGACACGGTCTCACGCGCCGGCGCCAACCACCACCACCACC
                                              535 AGCACGGGGGCTCGCCATGACCCAGGGCGGGCGGCAGCATCATCTCCGTCGCCAGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: PERSER, Claire M.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 2436-2007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILIAG DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             271 GCGGCCACGGCTTCGTGGTGCGCGAGACCAGGGTCGAAGAGGACATCAACACCTGCACCG
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49.8%; Pred. No. 0.34;
tive 0; Mismatches 122; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 49.8%
Matches 121; Conservative
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169 ACGCCGCCGCCGCCACCACCACCTCCTCAAGGAGAAGTTCGAGGAGGTCGACACGGTCT 228
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                   Pacquence 4, Application US/09249585A

Patent No. 6417002

GENERAL INFORMATION:
APPLICANT: HOLICK, ROBERT
ATTLEANT: HOLICK, ROBERT
TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISOMES
FILE REFERENCE: 0867/00905
CURRENT APPLICATION NUMBER: US/09/249,585A
CURRENT FILING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                                                          Score 47.2; DB 4; Length 1926;
Pred. No. 0.21;
0; Mismatches 123; Indels 0
                                                                                                                                                                                                                                                            NAME/KEY: misc_feature; LOCATION: (1)..(1926); OTHER INFORMATION: template strand of EBNA-1 DNA US-09-249-585A-4
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Job time: 81.4096 secs
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Best Local Similarity 49.6%;
Matches 121; Conservative
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ORGANISM: Epstein Barr Virus
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RESULT 15
US-09-249-585A-4/C
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LENGTH: 1926
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Human G-protein co Human DNA for pote Micromonospora DNA Human adenosine NA Mature isoamylase Flavobacterium iso Isoamylase gene.

AAV23640 AAT10428 AAV23639 AAF25795 AAF99682

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| SIDSZ/gcgdatu/geneseqn_embl/NA1980_DAT:*
| SIDSZ/gcgdatu/geneseq/geneseqn_embl/NA1981_DAT:*
| SIDSZ/gcgdatu/geneseq/geneseqn_embl/NA1991_DAT:*
| SIDSZ/gcdatu/geneseq/geneseqn_embl/NA2001_DAT:*
| SIDSZ/gcgdatu/geneseq/geneseqn_embl/NA2001_DAT:*
| SIDSZ/gcdatu/geneseq/geneseqn_embl/NA2001_DAT:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                    2185239 seqs, 1125999159 residues
                                                                nucleic - nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1:0
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Maximum DB seq length: 200000000
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574
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Randomising oligon PCR primer for 5' Sequence containin Oligo #7 for cloni Mycobacterium tube Mycobacterium tube DNA encoding G pro Human Orphan G pro Human G protein co
SUMMARIES	Query re Match Length DB ID	13 AAQ21833 14 AAQ36859 22 AAF76910 24 AAR7775 5 22 AAI99683 9 22 AAI99682 20 AAZ10560 21 AAD01125 21 AAA46026
	Length	390 390 390 390 4403765 4411529 1128 1128
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	Score	922225 22223225 922223 988
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New method of systematic polypeptide evolution by reverse translation – by linking each polypeptide in sample mixt, tindividualised mRNA allowing further synthesis of selected

WPI; 1992-080018/10.

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υ	42	47	8	2291	2.5		cype TGF-alph
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3 \$	0	ZEET-NOO	(III	(Ilrst entry)	_		
OE	Ran	Randomising	111901	oligonucleot1de		used in SPERT mRNA prepa	
X			•				
% & &	Sys	Systematic pouligand bindin	olype ng; sa	polypeptide eveding; ss.	evolution	ion by reverse translation; SPERT	т;
So	Syn	Synthetic.					
×	I						
N X	WO9	WO9202536-A.					
20	20-1	-FEB-1992.					
Y Y	01-7	01-AUG-1991;	916	91WO-US05463			
XX							
Z X	05-7	02-AUG-1990;	900	90US-0561968	. 89		
PA	(COLS	T'S ) ONIA	OF CC	OF COLORADO.			
PI	Gold	d L, Tuerk	k C;				
X	!						

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(GOLD/) GOLD L. (TUER/) TUERK C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-JAN-1992;
02-AUG-1990;
01-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US6194550-B1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAF76910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAF76910
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                                                                                                                                                                                                                                                                                                                                   283 TCGTGGTGCGCGAGACCAGGGTCGAAGAGGACATCAACACCTGCACCGGCGAGGTCCACG 342
                                                                                                                                                                                                                                                                                                                                                 163 GCCGCCACGGCGCGCGCGTCCAGCACGTCGTCAAGGAGAAGTTCGAGGAGGTCGACA 222
                                                                                                                                                                                                                                                                   168
                                      The sequence is that of an example randomising oligonucleotide which is used in the prepn. of mRNA encoding candidate polypeptides for the method of systematic polypeptide evolution by reverse translation (SPERT). The method provides a rapid way of isolating and identifying polypeptide ligands which bind to target mols. The polypeptide ligands can be used in e.g. assay methods, diagnostic procedures, cell sorting, as activators or inhibitors of target mol. function, as probes, as sequestering agents, drug delivery vehicles, modififers of hormone action and as catalysts. See also AAQ21830-Q21832.
                                                                                                                                                                                                          103 ACTACCAGGAGGTGGACTACTGCTCGGÀGGAGGTGAGGTCGGTGGCCCCGGCCGGCTTCG
                                                                                                                                                                                                                       223 CGGTCTCACGCGCCGGCGCCAACCACCACCACCATGGTCACCACGGCGGCGCCACGGCT
                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Systematic peptide evolution by reverse translation; SPERT; ligand; specific; inhibitors; probes; assay; cell sorting; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Systematic polypeptide evolution by reverse translation - used for prodn. of polypeptide ligand specific for desired target molecule
                                                                                                                                                                                       ö
                                                                                                                                                                 Query Match 10.9%; Score 62.6; DB 13; Length 390; Best Local Similarity 52.0%; Pred. No. 0.0016; Matches 140; Conservative 0; Mismatches 129; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCR primer for 5' fixed sequence contg. T7 promoter and RBS.
                                                                                                                                               Sequence 390 BP; 125 A; 126 C; 133 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                            349 ACGACGACGACGACGACGCCATGGTT 377
                                                                                                                                                                                                                                                                                                                                                                                343 AGCGCAGGGAGAGCTTCCTCGCCAGGGCT 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tuerk C;
                        Example; Page 55; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gold L, Pribnow D, Smith JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAQ36859 standard; DNA; 390 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91US-0739055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92WO-US00801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1993-076529/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-JAN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9303172-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAQ36859;
                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ36859
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SPERT is used to select novel polypeptides that bind the antibody of the epitope commonly recognised by the antisera from autoimmune at al., 1 Immunol. 144, 4613, 1990). The known epitope consists of ca. 10 amino acids at the N-terminus of the histone H2D consists of ca. 10 amino acids at the N-terminus of the histone H2D protein. To make mRNA encoding candidate polypeptides a 5' fixed protein. To make mRNA encoding candidate polypeptides a 5' fixed sequence composed of a 77 promoter sequence and a ribosome binding sequence composed of a 77 promoter sequence and a ribosome binding sequence composed of a 77 promoter sequence and a ribosome binding terminating in a restriction endouclease site is synthesised and cloned terminal trailer sequence of ca. 100 nucleotides lacking stop codons. The addition, a 3' primer annealing site is provided so that cDNA calborane complished on the mRNA recovered from partitioned calborane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103 ACTACCAGGAGGIGGACTACTGCTCGGAGGAGGIGAGGTCGGTGGCCCCGGCCGGCTTCG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     283 TCGTGGTGCGCGAGACCAGGGTCGAAGAGACATCAACACCTGCACCGGCGAGGTCCACG 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ligand isolation; systemic polypeptide evolution by reverse translation;
SPERT; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163 GCCGCCACGGCGGCGGCGTCCAGCACGTCGTCAAGGAGAAGTTCGAGGAGGTCGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    223 CGGTCTCACGCGCGGCGCCAACCACCACCACCATGGTCACCACGGCGCCCACGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence containing a 120 repeat of ACG flanked by fixed fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
10.9%; Score 62.6; DB 14; Length 390;
Best Local Similarity 52.0%; Pred. No. 0.0016;
Matches 140; Conservative 0; Mismatches 129; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 390 BP; 125 A; 126 C; 133 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          See also AAQ36845-63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 343 AGCGCAGGGAGGCTTCCTCGCCAGGGCT 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACGACGACGACGACGACGACGCATGGTT 377
Example 1; Page 84; 98pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92US-0829461.
90US-0561968.
91US-0739055.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAF76910 standard; DNA; 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ribosome complexes.
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us-10-090-035-3\_1.rng

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The present sequence was used in an example illustrating an invention relating to a method for isolating a polypeptide ligand for a desired target molecule. The method involves synthesising a nucleic acid mixture comprising mRNA having translatable each on-translatable regions and a mixture of nucleic acid polypeptide copolymers, each comprising the mRNA and a polypeptide encoded by its associated mRNA. The copolymers are partitioned relative to their affinity to the target. The method is termed systemic polypeptide evolution by reverse translation (SPERT). The polypeptide signal molecule targets are useful in assay methods, diagnostic procedures, cell sorting, as inhibitors of target. Normone action and have therapeutic uses as sequestering agents. The target molecules include natural and synthetic polymers, including proteins, hormones, receptors and cell surfaces, nucleic acids and small collecules such as drugs, metabolites, cofactors and toxins. Polypeptide and rapidly identified by this method.
                                                                                                                                                      Isolating a polypeptide ligand to a target molecule, useful for diagnostic assays, comprises partitioning candidate mixtures comprised of thosome complexes or mRNA.polypeptide copolymers relative to the target molecule
                                                                           Smith JD;
                                                                                                                                                                                                                                                                   Example; Column 39; 35pp; English.
                                                                    Tuerk C, Pribnow D,
                                                                                                              WPI; 2001-243412/25.
    (PRIB/) PRIBNOW D. (SMIT/) SMITH J D.
                                                                    Sold L,
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223 CGGTCTCACGCGCCGCGCGCCAACCACCACCACCATGGTCACCACGGCGGCGCCACGGCT 282 283 TCGTGGTGCGCGAGACCAGGGTCGAAGAGGACATCAACACCTGCACCGGCGAGGTCCACG 342 163 GCCGCCACGCGCGCGCGTCCAGCACGTCGTCAAGGAGAAGTTCGAGGAGGTCGACA 0; Gaps Query Match 10.9%; Score 62.6; DB 22; Length 390; Best Local Similarity 52.0%; Pred. No. 0.0016; Matches 140; Conservative 0; Mismatches 129; Indels 0; Sequence 390 BP; 125 A; 126 C; 133 G; 6 T; 0 other; 343 AGCGCAGGGAGAGCTTCCTCGCCAGGGCT 371 g ò 셤 õ 8 ð g ö

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T7 promoter; ribosome binding site; RBS; prokaryotic; eukaryotic; ribosome; mRNA.circle-solid.polypeptide copolymer; mRcs.pC; SPERT; Systematic Polypeptide Evolution by Reverse Translation; assay; diagnosis; cell sorting; inhibitor; probe; sequestering agent;
                                                                                                                              Oligo #7 for cloning T7 promoter and RBS containing mRNA.
                               AAI72775 standard; DNA; 390 BP
                                                                                               22-JUL-2002 (first entry)
                                                                 AAI72775;
RESULT 4
               AAI72775
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ribosome complex; ss.

349 ACGACGACGACGACGACGCCATGGTT 377

a

The sequences given in AA172769-81 are oligonucleotides which were used to make mRNA encoding a candidate polypeptide, a 5' fixed sequence composed of a 77 promoter sequence and a ribosome binding site which is recognised by both prokaryotic and eukaryotic ribosomes, terminating in a restriction endonuclease site. The resulting nucleic acid was used in a restriction endonuclease site. The resulting nucleic acid was used in the method of the linvention for preparing ligands of target molecules complexes or mRNA.circle-solid.polypeptide in which mixtures of ribosome complexes or mRNA.circle-solid.polypeptide copolymers (mRcs.pCs) are partitioned by affinity to the target and amplified to create candidate mixtures enriched in ribosome complexes or mRCs.pCs with an affinity to the target, are new. The methods are useful for isolating polypeptide in ribosome complexes or mRcs.pCs with an affinity to the target, are new. The methods are useful for isolating protecting polypeptide products are useful for assay methods, diagnostic procedures, cell sorting, as inhibitors of the aspert methods diagnostic procedures, cell sorting, as inhibitors of target molecule function, as probes, as sequestering agents and the carget molecule function, as probes, as sequestering agents and the carget molecule and protectins, polysaccharides, glycoprotectins, bormones, clarget molecule sinclude natural and synthetic polymers, including protectis, polysaccharides, glycoprotectins, bormones, creeptors and cell surfaces, nucleic acids, and small molecules such acts as manageds and the novel SPERT method involves utilizing a candidate polypeptides are copypeptides having a randomized amino acid sequence. Each member of the mixture is linked to an individualized mNNA, which encodes the partitioned according to their property of binding to append according to their property of binding to agree and the mRNA encoding a polypeptide is partitioned each mixture of the mixture is linked to an individualized of the copypeptide and the mRNA encoding New methods (termed SPERT (Systematic Polypeptide Evolution by Reverse Translation)) for selecting high-affinity polypeptide ligands that specifically bind target molecules, e.g. proteins, carbohydrates, toxins, drugs and receptors Smith JD; Example 1; Page 21; 38pp; English. Tuerk C, Pribnow D, 98US-0197649. 90US-0561968. 91US-0739055. 22-FEB-2001; 2001US-0790399. WPI; 2002-329128/36. (GOLD/) GOLD L. (TUER/) TUERK C. (PRIB/) PRIBNOW D. (SMIT/) SMITH J D. US2002038000-A1. 01-AUG-1991; 8-MAR-2002. 23-NOV-1998; 02-AUG-1990; Synthetic. Gold L, 

10.9%; Score 62.6; DB 24; Length 390; 52.0%; Pred. No. 0.0016; 1.ve 0; Mismatches 129; Indels 0. Sequence 390 BP; 125 A; 126 C; 133 G; 6 T; 0 other; Query Match 10.9 Best Local Similarity 52.0 Matches 140; Conservative

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Gaps

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Length 4403765;

22; 98;

DB

Score 53.2; DB Pred. No. 0.28; Mismatches

9.38;

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112; Conservative

Query Match Best Local Matches

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Indels

207 ITCGAGGAGGTCGACACGGTCTCACGCGCCGCGCCCAACCACCACCACCACCATGGTCAC

326

147 GCCCCGGCCGGCTTCGGCCGCCGCGCGCGCGCTCCAGCAGCACGTCGTCAAGGAGAAG

1191389 GGCGCCAACGCCGGCAACGCCGCAACGGC 1191360

327 ACCGGCGAGGTCCACGAGCGCAGGGAGAGC

CACGGCGGCCACGGCTTCGTGCTGCGCGAGACCAGGGTCGAAGAGGACATCAACACCTGC

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168
                                                           222
                                                                                                                      282
                                                                                                                                        342
                                                                                                                                                                                                 The invention relates to evaluating strain variation within and between different populations of the tuberculosis bacterial pathogen.
Mycobacterium tuberculosis or related Mycobacterium by determining the nucleotide sequence of the first strain at positions in the complete sequence of the genome that correspond to positions that differ in the nucleotide sequences of M. tuberculosis strains COC 1551 (AAI99683) and H37Rv (AAI99682). The method is useful for evaluating strain variation G. tuberculosis and has valuable application in the fields of tuberculosis genetics, epidemiology, patient treatment and epidemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Evaluating strain variation of Mycobacterium tuberculosis, comprises determining the nucleotide sequence of the strain at positions in the genome corresponding to positions where M. tuberculosis strains CDC 1551 and H37Rv differ
ACTACCAGGAGGIGGACTACTGCTCGGAGGAGGIGAGGICGGTGGCCCCGGCCGGCTTCG
                            GCCGCCACGGCGGCGGCGTCCAGCACGTCGTCAAGGAGAAGTTCGAGGAGGTCGACA
                                                                                        TCGTGGTGCGCGAGACCAGGGTCGAAGAGGACATCAACACCTGCACCGGCGAGGTCCACG
                                                                                                                        CGGTCTCACGCGCCCCCAACCACCACCACCACCATGGTCACCACGGCGCCACGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis; strain H37Rv; strain CDC 1551; genome; variation; epidemiology; patient treatment; epidemic monitoring; d
                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis strain H37Rv genome SEQ ID NO 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; SEQ ID NO 2; 3pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Venter JC;
                                                                                                                                                                                                                                              343 AGCGCAGGGAGAGCTTCCTCGCCAGGGCT 371
                                                                                                                                                                                                                                                                           ACGACGACGACGACGACGCCATGGTT 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fraser CM,
                                                                                                                                                                                                                                                                                                                                        AAI99683/c
ID AAI99683 standard; DNA; 4403765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENOMIC RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-647261/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fleischmann RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GENO-) INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US6294328-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-JUN-1998;
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      103
                                    601
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                                                                                                                              223
                                                                                                                                                                                                                                                                                                                                                                                      AA199683
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to evaluating strain variation within and between different populations of the tuberculosis bacterial pathogen.

Mycobacterium tuberculosis or related Wycobacterium by determining the nucleotide sequence of the first strain at positions in the complete sequence of the genome that correspond to positions that differ in the nucleotide sequences of M. tuberculosis strains CDC 1531 (AA199683) and H37Rv (AA199682). The method is useful for evaluating strain variation of M. tuberculosis and has valuable application in the fields of tuberculosis genetics, epidemiology, patient treatment and epidemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4411529 BP; 758565 A; 1449983 C; 1444602 G; 758379 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ωναιυατιπg strain variation of Mycobacterium tuberculosis, comprise determining the nucleotide sequence of the strain at positions in th genome corresponding to positions where M. tuberculosis strains CDC 1551 and H37Rv differ
                                                                                                                                                 Mycobacterium tuberculosis; strain H37Rv; strain CDC 1551; genome; variation; epidemiology; patient treatment; epidemic monitoring; ds
                                                                                                                   strain H37Rv genome SEQ ID NO 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 1; 3pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                        Venter JC;
                                                                                                                                                                                                                                                                                                                                                                                                                          Fraser CM,
               BP.
             AA199682 standard; DNA; 4411529
                                                                                                                                                                                                                                                                                                                      98US-0103840.
                                                                                                                       Mycobacterium tuberculosis
                                                                                                                                                                                                              Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                              White OR,
                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                          (GENO-) INST GENOMIC RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-647261/74.
                                                                                                                                                                                                                                                                                                                                                                                                                            Fleischmann RD,
                                                                                                                                                                                                                                                                                                                      24-JUN-1998;
                                                                                     15-JAN-2002
                                                                                                                                                                                                                                                                                    25-SEP-2001.
                                                    AAI99682;
AA199682
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jo

Sequence 4403765 BP; 757105 A; 1447799 C; 1441301 G; 757371 T; 189 other;

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at segdata.uspto.gov/sequence.html?DocID=6294328B1..

monitoring.

662 216

603

543

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97 TGGCTTACTACCAGGAGGTGGACTACTGCTCGGAGGAGGTGAGGTCGGTGGCCCCGGGCCG 156
                                                                                                        217 TCGACACGGTCTCACGGGCCGGCCGACCACCACCACCACCATGGTCACCACGCGGGC 276
                                                                                                                                                  277 ACGGCTTCGTGGTGCGCGAGACCAGGGTCGAAGAGGACATCAACACCTGCACGGGGAGG 336
                                                                                                                                                                 542 GGGCGCCCTCTGCTCCAGGCCCACCTCCTCGTCGTCGTCGCCACGCCG 483
                                                                                                                                                                                                                                                                                                                                                               Human; orphan G protein-coupled receptor; GPCR; hGPCR27; drug screening;
transmembrane receptor; expressed sequence tag; EST; signal cascade; ss.
                                     721 FGGCGGCCGCCTGGCGCCCGGCCGTGAAGTCCAGTCGTGGCTGACGCGG
                                                                                                                     GCTTCGGCCGCCACGCGGCGCGTCCAGCACCACGTCGTCAAGGAGAAGTTCGAGGAGG
                                                                              /note= "Human orphan G protein-coupled receptor"
                                                                                                                                                                                                                                                                                                                                           Human orphan G protein-coupled receptor hGPCR27 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1..1128
/*tag= a
/product= "hGPCR27"
                                                                                                                                                                                              TCCACGAGGGCAGGGAGAGC 356
                                                                                                                                                                                                                  TCCAGCACTGGCGGGAAGGC 463
                                                                                                                                                                                                                                                                             BP
                                                                                                                                                                                                                                                             AAD01125/c
ID. AAD01125 standard; cDNA; 1128
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99US-0123949
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99US-0417044
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28-MAY-1999;
28-MAY-1999;
28-MAY-1999;
28-MAY-1999;
                                                                                                                                                                                                                                                                                                                    02-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-JUN-2000
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                                                                                                                                                                                                                                                     RESULT 8
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                                                                                                                                            3932848 CGGGGGACAAGGCGGGGGCGCGGGGGGCGGGGGCGGATAACCCCACGGCAT 3932907
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                                                                                     209 CGAGGAGGICGACACGGICTCACGCGCCGGCGCCAACCACCACCACCATGGICACCA 268
                                                                                                                                CGGGGGCACGCTTCGTGGTGCGCGAGACAGGGTCGAAGAGGACATCAACACCTGCAC 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ij
                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G protein-coupled receptor proteins expressed in the central nervous system and genes encoding them -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence encodes a G protein-coupled receptor protein, designated SRBB1. The protein is expressed in the central nervous system. The SRBB products are used for the diagnosis and treatment of diseases of the central nervous system, including inflammatory disorders of immunological origin.
  Score 53.2; DB 22; Length 4411529;
Pred. No. 0.28;
0; Mismatches 88; Indels 0; G
                                                                                                                                                                                                                                                                                                                                           G protein-coupled receptor protein; SREB1; central nervous system;
inflammatory disorder; immunological; ss.
                                                                                                                                                                                                                                                                                                                     DNA encoding G protein-coupled receptor protein designated SREBI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
9.2%; Score 52.8; DB 20; Length 1128;
Best Local Similarity 52.7%; Pred. No. 0.15;
Matches 137; Conservative 0; Mismatches 122; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kamohara M;
                         88; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1128 BP; 116 A; 437 C; 395 G; 180 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matsumoto M, Sugimoto T, Takasaki J, Saito T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 47-49; 72pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1..1128
/*tag= a
/product= "SREB1"
                                                                                                                                                                                                                                        AAZ10560/c
ID AAZ10560 standard; DNA; 1128 BP.
                                                                                                                                                                                      3932908 CGCCGCCCCCC 3932921
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9.3%;
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                                                                                                                                                                            CGGCGAGGTCCACG 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-JP01191.
                                                                                                                                                                                                                                                                                              15-NOV-1999 (first entry)
      Best Local Similarity 54.69
Matches 106; Conservative
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P-PSDB; AAY30532.
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03-FEB-1999;
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Ouery Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                277 ACGCCTTCGTGGTGCGCGAGACCAGGGTCGAAGAGGACATCAACACCTGCACCGGCGAGG 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               542 GGGCGCCGTCGCCCCTGCTCCAGGCCCACCCCTCCTCGTCGTCGTCCACCCCC 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          603
                                                                                                                                                                                                                                                                                                                                                                                                                                     orphan G protein coupled receptor (GPCR), expressed in foetal brain, putamen, pituitary gland and caudate nucleus. The hGPCR27 CDNA was identified using EST (expressed sequence tag) AA778870 as a probe. The orphan GPCR of the invention, like all GPCRs has seven transmembrane alpha helices with an extracellular N-terminus and an intracellular C-terminus. However, no endogenous ligands has yet been identified for the proteins of the invention. The orphan GPCRs may be used in the identification of their endogenous ligands, and to screen potential GPCR agonists and antagonists for use as pharmaceutical agents. The proteins may also be used in the study of GPCR-mediated signalling cascades, and to elucidate their precise role in normal and diseased human conditions. Nucleic acid encoding human orphan GPCRs may be used for tissue formation expression analysis to provide information about their formation about their formation about their formation and their formation and their formation about their formation and their formation about their formation and the formation and their formation are and the formation and their formation are and the formation and their formation are also and the formation are and the formation and their formation are and the formation and their formation and their formation are and the formation are and the formation and their formation are and the formation and their formation are and the formation and their formation are and the formation and the formation are and the formation are and the formation and the formation and the formation are and the fo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            157 GCTTCGGCCGCCACGGCGGCGGCGTCCAGCACGTCGTCAAGGAGAAGTTCGAGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             661 GCACCAGGCGCGCGGGCCGCATCTTGCGGC-GGTCGTGGATGAAGAAGAGCAGGCGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   602 TAGACGAGGTGCGTGGCGCCCACCACCACGGCCAGCAGCAGCAGGAAGCCCAGCGCCCG
                                                                                                                                                                                                                                                 Novel human orphan G protein-coupled receptors and the encoding cDNAs for use in the identification of G protein-coupled receptor agonists .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human G protein coupled receptor hGPCR27 encoding cDNA SEQ ID NO:17
                                                                                                                                                                                                                                                                                                                                                                                                                       present sequence is a CDNA encoding hGPCR27, an endogenous human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; G protein coupled receptor; GPCR; transmembrane receptor; identification; agonist; screening; therapeutic; pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 52.8; DB 21; Length 1128; Pred. No. 0.15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1128 BP; 116 A; 437 C; 395 G; 180 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       function in healthy and pathological states.
                                                                                                                                                                                                                                                                                                                                                         Claim 29; Page 61-62; 102pp; English
                                                                                          Lin I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                337 TCCACGAGCGCAGGGAGAGC 356
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52.7%;
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                     (AREN-) ARENA PHARM INC.
                                                                                                                                                   WPI; 2000-400068/34.
P-PSDB; AAY71298.
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                                                                                      Dang HT,
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The present invention describes transmembrane receptors, preferably human G protein coupled receptors (GPCR), for which the endogenous ligand is unknown (orphan GPCR receptors). More specifically the present invention relates to non-endogenous, constitutively activated versions of a human GPCR. These non-endogenous human GPCRs can be useful for the direct identification of candidate compounds as receptors agonists, inverse agonists or partial agonists for use as pharmaceutical agents. AAA46017 to AAA46126 and AAB02855 to AAB02859 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      542 ececicarcercecrecrecrecrecedecececececerercercercercecece 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dang HT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1128;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.2%; Score 52.8; DB 21;
52.7%; Pred. No. 0.15;
tive 0; Mismatches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lehmann-Bruinsma K, Chalmers DT, (iaw CW, Lin I, Lowitz K, White C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 91-92; 187pp; English.
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Gore M, Liaw CW, Lin I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AREN-) ARENA PHARM INC.
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Matches 137; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAB02832.
13-0CT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a method of identifying an agent that binds to and/or modulates activity of human G-protein coupled receptor (GPCR) 14266. The invention also provides a method for modulating the level or activity of the GPCR in cells in vivo or in vitro, or in a subject predisposed to having a haematopoletic or neutrophil deficiency disorders. Detecting 14266 polypeptides or nucleic acids in specific conjugical samples is useful in disease diagnosis. Modulating level or activity of the GPCR polypeptide or polynucleotide is useful for treating spleen (e.g. splenomegaly, neoplasms); lung (e.g. vlainmonary hypertension, complysems); colon (e.g. diarrhoea and dysentery, idiopathic inflammatory cendometrium (e.g. endometrials); utral hepatitis); uterus and conte meningitis, multiple sclerosis, spinocerebellar degeneration); cacute meningitis, multiple sclerosis, spinocerebellar degeneration); crells (e.g. systemic lupus erythematosus, polyarteritis nodosa); skin (e.g. vittiligo, acanthosis nigricans); heart (e.g. heart failure,
                                                                                                                                                                               Human; G-protein coupled receptor; GPCR 14266; haematopoietic disorder; neutrophil deficiency disorder; splenomegaly; pulmonary hypertension; colon; diarrhoea; hepatic injury; idiopathic inflammatory bowel disease; uterus; endometriosis; brain; acute meningitis; multiple sclerosis; T-cell; systemic lupus erythematosus; skin; vitiligo; heart failure; angina pectoris; atherosclerosis; haemolytic anaemia; thymic cyst; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying compound that binds to and/or modulate activity of the polypeptide for treating splenomegaly, emphysema and multiple sclerosis, comprises using human G-protein coupled receptor 14266
                                                                                                                                                                                                                                                                                                                                                         /*tag= b
103..1125
/*tag= c
/product= "Mature GPCR 14266"
                                                                                                                                                            Human G-protein coupled receptor 14266 DNA.
                                                                                                                                                                                                                                                                                                                      /*tag= a
/product= "GPCR 14266"
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1..1128
  TCCACGAGCGCAGGGAGAGC 356
                   AAD27892 standard; DNA; 1128 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MILL-) MILLENNIUM PHARM INC.
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                                                                                                                                  31-MAY-2002 (first entry)
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P-PSDB; AAE14597.
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                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                        AAD27892,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       542 GGGGCGCCGTCGGCCGCTCCAGGCGCACGCGCGTCCTCGTCGTCGCCACCGCG 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; G protein-coupled receptor; GPCR; ds; GAL4; galanin receptor; databaler's disease; amyotrophic lateral sclerosis; asthma; atherosclerosis; basal cell carcinoma; breast carcinoma; cardiomyopathy; chondrosarcoma; chronic obstructive pulmonary disease; Crohn's disease; multiple sclerosis; osteoarthritis; osteoprosis; parkinson's disease; pooriasis; rheumatoid arthritis; schizophrenia; ulcerative colitis; tuberculosis; cognition disorder; memory disorder; anorexia; hormonal release disorder; cardiovascular activity disorder; pain perception disorder; disobetes; obesity; diabetes; obesity; diabetes; hyperlipidaemia; stroke; gene therapy.
angina pectoris); blood vessels (e.g. atherosclerosis, Raynaud disease, thalassaemia syndromes, haemolytic anaemia) and disorders of the thymus (e.g. thymic cysts, Hodgkin's disease). The present sequence is human GPCR 14266 DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel G protein-coupled receptor polypeptides including galanin receptor polypeptides useful for identifying modulators that are useful
                                                                                                                                                                                                                                                                                                                             721 TGGCGGCCGCTGGCCGGTGGCCCGGGCCGTGGAAGGTCCAGTCGTGGCTGACGCGG
                                                                                                                                                                                                                                                                                                                                                                                157 GCTTCGGCCGCCACGGCGGCGGCGTCCAGCACGTCGTCAAGGAGAAGTTCGAGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                TCGACACGGTCTCACGCGCCGCGGCGCCAACCACCACCACCATGGTCACCACGGCGCC
                                                                                                                                                                                     Length 1128;
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                                                                                                                       Sequence 1128 BP; 116 A; 437 C; 395 G; 180 T; 0 other;
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                                                                                                                                                                             Score 52.8; DB 24;
Pred. No. 0.15;
); Mismatches 122;
                                                                                                                                                                                DB 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brown JP, Miller M, Burmer G, Fabre-Suver C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             337 TCCACGAGCGCAGGGAGAGC 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                Best Local Similarity 52.7
Matches 137; Conservative
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Best Local S
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//note= "No start codon"
complement (12108..13022)
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complement (13027..13030)
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complement (17870..18934)
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complement 16419..17873
                                       Micromonospora carbonacea var. africana.
                                                                                                                                                                                                                                                                                                                                                                                                              complement (3867..3870)
                                                                                                                                                                                                                              complement (1490..2611)
                                                                                                                                                                                                                                                                       /product= "EvdB"
complement (2618..2622)
                                                                                                                                                                                                                                                                                                                                              complement (2622..3860)
                                                                                                                                                                               complement (1389..1394)
                                                                                     Location/Qualifiers
complement (132..1382)
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product= "EvdJ"
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                                                                                                                                                    'product= "EvdA"
                                                                                                                                                                                                                                                                                                                                                                                            "EvdC
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4..11176
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fermentation; ds.
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                                                                                                                                                                                                                                                                                                       RBS
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                                                                                                      The invention relates to an isolated polypeptide encoded by a nucleic acid molecule that is at least 80% identical to the G nucleic acid molecule that is at least 80% identical to the G rucleic acid molecule that is at least 80% identical to the G protein-coupled (GPCR) polynucleotides included in the specification.

CC Also included are probes based on the GPCR sequences (including antisense probes), a host cell comprising an expression vector comprising can methods of identifying modulators of the polypeptides. The polypeptides are useful for identifying modulator compounds which compounds which is a modulators, activators, repressors, agonists or antagonists of the propeptides and nucleic acid probes as described above can be used to detect the presence of the polypeptides and nucleic acid searched in which GPCRs are involved compounds and area to dispenses a variaty of diseases or disporaters in which GPCRs are involved componsarroma, chronic obstructive pulmonary disease, cohonforsarroma, chronic obstructive pulmonary disease, cohonforsarroma and arthitis, schizophrenia ulcerative colitis, tuberculosis and many other diseases listed in the specification. The probes and antibodies are also useful for diagnosing cognition and memory disorders, many near many mentonicy disorders. Anonexia, hormonal release disorders, cardiovascular activity disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     277 ACGGCTTCGTGGTGCGCGAGACCAGGGTCGAAGAGACACATCAACACCTGCACCGGCGAGG 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97 TGGCTTACTACCAGGAGGTGGACTACTGCTCGGAGGAGGTGAGGTCGGTGGCCCCGGCCG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  602 TAGACGAGGTGCGTGGCGCCCACCACGACGAGCAGCAGGAAGCCCAGCGCGCCG 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disorders, pain perception disorders, obesity, diabetes, Alzheimer's disease. Preferably, compounds that decrease or increase the expression of galanin receptor (GAL4) can be used to treat obesity, diabetes, hyperlipidaemia and stroke. The GPCR nucleic acid is useful for treating the above mentioned disorders by gene therapy techniques. The present sequence is a novel GPCR polynucleotide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   157 GCTTCGGCCGCCACGGCGGCGGCGTCCAGCACGTCGTCAAGGAGAAGTTCGAGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                721 TGGCGGCCGCCTGGCCGCTGGCGCCCTGGAAGGTCCAGTCGTGGCTGACGCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               217 TCGACACGGTCTCACGCGCCGCGCGCCAACCACCACCACCACCATGGTCACCACGGCGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Micromonospora DNA encoding biosynthetic enzymes for Everninomycin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
       for treating Alzheimer's disease, psoriasis, melanoma, multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 52.8; DB 24; Length 1128;
Pred. No. 0.15;
0; Mismatches 122; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Everninomicin; antibiotic; bottle-neck gene; orthomicin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1128 BP; 116 A; 437 C; 395 G; 180 T; 0 other;
                                                                           Disclosure; Page 116-117; 144pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    337 TCCACGAGCGCAGGGAGAGC 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   482 TCCAGCACTGGCGGGAAGGC 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAS08693 standard; DNA; 109519 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 9.2%;
Best Local Similarity 52.7%;
Matches 137; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nvention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAS08693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAS08693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
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1937420906 /*tag= z / product= "EvrE" 2106422542 /*tag= aa / product= "EvrE" 210562242 /*tag= ab / 2274824172 /*tag= ab / 2274824172	/*tag ad complement (2417725223) /*tag ae /*tag ae /*product "EvrH" complement (2523025233) /*tag af 2555026626 /*tag af /*product "EvrI" 2668530479 /*tag ah	*tag= al onclement (3055731 onclement (3055731 product= "EvrK" omplement (3188531 *tag= ak onclement (3194132 product= "EvrL" onclement (3316734 tag= am product= "EvrM" tag= am		/product= "EvrR" complement (3889240163) /*tag= au /product= "EvrS" complement (4021640890) /*tag= av /product= "EvrT" complement (4089940902) /*tag= av /product= "EvrU" complement (4088741576) /*tag= av /product= "EvrU" complement (4167942707) /*tag= az complement (4271442717) /*tag= az complement (4271442717) /*tag= az complement (4271442717)
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RBS CDS CDS CDS RBS RBS	CDS CDS CDS CDS CDS CDS	CDS CDS CDS CDS CDS CDS	Query Match Best Local Matches 14 7 106	166 11872 226 11932	286 11992 346 <sup>-</sup> 12052	406
			ON NO O	oy oy oy	6	Qy Db

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The specification describes antisense oligonucleotides (AAX52869-X55271)

directed against at least 2 mRNAs selected from target genes, coding and non-coding regions of RNAs corresponding to target genes, coding and non-coding regions, intron-exon borders, the intration codons, genomic flanking regions, intron-exon borders, the silend, the 3'-end and the juxta-section between coding and non-coding comparison of RNAs encoding proteins associated with one or more diseases, conditions or mixtures. The antisense oligonucleotides may be derived from sequences AAX55272-74. These multiple target conjugated specifically AAX5180-271) can be used for the antisense treatment of diseases and conditions. Typical diseases and conditions are those associated with impaired respiration and including lung diseases, pulmonary vasoconstriction, inflammation, including lung diseases, pulmonary vasoconstriction, confit in a larget chinitis, acute asthma, allergies, asthma, impeded confirmant bull of the sease (OPD), and cancers such as leukemias, lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer, lepatic metastasized to the lungs, including breast and prostate cancer.
                                                                                                                                                                                                                                              pulmonary vasconstriction; inflammation; allergic rhinitis; acute asthma; allergy; asthma; impeded respiration; respiration; allergy; asthma; impeded respiration; respiration; pulmonary distress syndrome; pain; cystic fibrosis; pulmonary hypertension; pulmonary vasoconstriction; emphysema; chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma; colon cancer; breast cancer; lung cancer; pancreatic cancer; hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antisense oligonucleotides used in treatment of, e.g. pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 114955 BP; 6071 A; 29417 C; 36712 G; 21328 T; 21427 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 9.2%; Score 52.8; DB 20; Length 114955; Best Local Similarity 35.6%; Pred. No. 0.24; Matches 144; Conservative 29; Mismatches 232; Indels 0;
                                                                                                                                                                                                             antisense treatment;
                                                                                                                                                                   Human adenosine Al receptor antisense oligonucleotide fragment.
                                                                                                                                                                                                          Antisense oligonucleotide; multiple target; antis
impaired respiration; inflammation; lung disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 37; 120pp; English.
                                       AAX53491 standard; DNA; 114955 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98WO-US19419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0093972,
97US-0059160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYEC-) UNIV EAST CAROLINA
                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-229400/19
                                                                                                                                                                                                                                                                                                                                                                                                  prostate cancer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vasoconstriction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-JUN-1998;
                                                                                                                         05-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9913886-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                               AAX53491;
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RESULT 13
                      AAX53491
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103187 CCAVGACGCCGCGCNNHNNNSCCGGCCCGACGCCGCCAVGACGCCGCGCNHNNNSCC 103128
103308
                                                                                                                                                                                                                                                              103247 CCGCGCNNHNNNSGGCCCGACGCCCAVGACGGCCGCGCNNHNNNSCGGCCCGACGCC 103188
                                                                                                                                                                                                                                                                                             360
                                                                                                                                                                      240
                                                                                                                            181 TCCAGCAGCACGTCGTCAAGGAGAAGTTCGAGGAGGTCGACACGGTCTCACGCGCCGGCG
                                             GGCGCTGCGCACAGACACCAAGCGTCGGCACCAATGGCTTACTACCAGGAGGTGGACT
                                                                                                          121 ACTGCTCGGAGGAGGTGAGGTCGGTGGCCCCGGCCTTCGGCCGCCGCCACGGCGGCGCG
                                                                                                                                                                                                                                  241 CCAACCACCACCACCACGATCACCACGGCGGCCACGGCTTCGTGGTGCGCGAGACCA
                                                                                                                                                                                                                                                                                             301 GGGTCGAAGAGGACATCAACACCTGCACCGGCGAGGTCCACGAGCGCAGGGAGAGCTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A DNA sequence (AAT10429) codes for the mature isoamylase (plus an N-terminal methionine) of Flavobacterium sp. (see also AAR92692). It was obtd. by amplification of the cloned isoamylase gene (AAT10428) using primers (AAT10423.33) designed to add a start codon to the beginning of the processed mature enzyme (Ala-33) and a stop codon adjacent to the endogenous TGA codon. The DNA sequence is used for the recombinant prodn. of isoamylase or can be expressed in transgenic plants, e.g. potato, cassava, sweet potato, corn, wheat, barley or rice, to alter the amylose:amylopectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated DNA encoding isoamylase - used to produce plants having a modified starch content, e.g. a higher ratio of amylose to
                                                                                                                                                                                                                                                                                                                                                                           103127 CGCCCCGACGCCCCAVGACGCCGCGCNNHNNNSGCCCGGCCCG 103083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isoamylase; starch; amylose; amylopectin; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                          361 TCGCCAGGGCTAACTGAGCCGCCCGGCGGCGGCATCCACGCCCG 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2; Page 35-39; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Krohn BM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT10429 standard; DNA; 2244 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95WO-US09323.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Barry GF, Kishore GM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mature isoamylase DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MONS ) MONSANTO CO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Flavobacterium sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9603513-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-JUN-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fructose;
                                                  61
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                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
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151 CGGCCGGCTTCGGCCGCCACGGCGGCGCGTCCAGCAGCACGTCGTCAAGGAAGTTCG
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                                                                   211 AGGAGGTCGACACGGTCTCACGCGCCGGCGCCAACCACCACCACCACCATGGTCACCACG
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Job time : 214.272 secs
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                                                                                                                                                           211 AGGAGGTCGACACGGTCTCACGCGCCGGCGCCAACCACCACCACCACCATGGTCACCACG 270
                                                                                                                                                                                                               271 GCGGCCACGGCTTCGTGCGCGAGACCAGGGTCGAAGAGACATCAACACCTGCACCG 330
                                                                                                        151 CGGCCGGCTTCGGCCGCCACGGCGGCGGCGTCCAGCAGCACGTCGTTCG 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence encodes the Flavobacterium isoamylase of the invention. The protein can be used to produce higher amylose starches, using genetically modified plants.
                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
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                                                   Ouery Match 9.0%; Score 51.8; DB 17; Length 2244; Best Local Similarity 54.5%; Pred. No. 0.25; Matches 104; Conservative 0; Mismatches 87; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
9.0%; Score 51.8; DB 19; Length 2244;
Best Local Similarity 54.5%; Pred. No. 0.25;
Matches 104; Conservative 0; Mismatches 87; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA coding for Flavobacterium isoamylase - for production of recombinant isoamylase or transgenic plants
                          Sequence 2244 BP; 427 A; 827 C; 704 G; 286 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2244 BP; 427 A; 828 C; 703 G; 286 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isoamylase; high amylose starch production; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Flavobacterium isoamylase coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; Column 27-32; 20pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1..2241
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Barry GF, Kishore GM, Krohn BM;
                                                                                                                                                                                                                                                                                                                                                               AAV23640 standard; DNA; 2244 BP
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94US-0281902.
                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                             2057 GCGCGGTCGAC 2067
                                                                                                                                                                                                                                                                    GCGAGGTCCAC 341
ratio of the starch.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MONS ) MONSANTO CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-296898/26.
P-PSDB; AAW53886.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Flavobacterium sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JUN-1995;
28-JUL-1994;
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OM nucleic - nucleic search, using sw model	
Run on: June 15, 2003, 23:43:51; Search time 1684.35 Seconds (Without alignments) 9917.805 Million cell updates/sec	
Title: US-10-090-035-3 Perfect score: 574 Sequence: 1 acccacgcytccgcccacgcaaaaaaaaaaaaaaa 574	
Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0	
Searched: 2054640 seqs, 14551402878 residues	
Total number of hits satisfying chosen parameters: 4109280	
Minimum DB seq length: 0 Maximum DB seq length: 2000000000	
Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	
3: 95_10:4 4: 95_0m:* 5: 95_pat:* 7: 95_ph:* 8: 95_pl:* 10: 95_r:* 11: 95_r:* 11: 95_rs:* 13: 95_un:* 14: 95_un:* 15: 95_un:*	
3/: em_htg_vrt:* 39: em_gy;* 39: em_htgo_hum:* 40: em_htgo_mus:* 41: em_htgo_other:*	

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Š	Sco	Query Match	Į,	DB	D	Description	uo
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U U	174	30.4	173699	ω (	AP003416	03416	Oryza sa
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	57	0	184	-			Strepton
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	ν. 1	4.	1464	~	375		Oryza sa
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4 -	7.	0.6	224	9	AR007590		Sequence
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C 44	51.	6 0 0	3853	-	SCE94		trent
45	51.	0.6	14925	~	P00	APOURA O	

## ALIGNMENTS

PLN 17-MAY-2002 chromosome 1,	onbare) DNA,	racheophyta;	
linear Pi genomic DNA, cl	(cultivar:Nippo	Embryophyta; 1	
AP003416 173699 bp DNA 11near PLN 17-MAY-Oryza sativa (japonica cultivar-group) genomic DNA, chromosome AP003416 AP003416 GI:20804922	Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA, clone:P0456E05.	Oryza sativa (japonica cultivar-group) Eukaryots, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Maqnolitophyta; Lilionsida; Poales: Passes	Ehrhartoideae; Oryzeae; Oryza. 1
RESULT 1 AP003416/C LOCUS DEFINITION ACCESSION VERSION KEYWORDS	SOURCE	ORGANISM	REFERENCE

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OEISETSSRVEYDDPSQLEVDRDEDYRSEADVSNGTFGYKPHIEELEMILLEAYFVQI
DGTLNKLSHLREYVDDTEDYINIMLDDKONQLLQMGVMLSTATVVITAGYAVVGLFGM
NIGISLYADPTNREERRASNMKFWETHLGTIAGGTVWTIVAMGWGKRSGLLQ"
Join (1697) 37082, 37255. 37479, 37601, 37701, 37823. 38015,
38424. 38764, 59169. 39399, 39493. 39645)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     join(36977. .37082,37255. .37479,37607. .37701,37823. .38015,
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                                                                                                                               .21058,21870. .22177,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MVVLKIKGKDEAGRUNRIWHWGINASSVLSVYTAAAVRIVHNASVYHFFDAM"
complement(join(40277. .40417,40717. .40773,40875. .41073,
41173. .41300,41399. .41504,41677. .41756,42145. .42242,
42324. .42437,42523. .42663,42757. .42841,43717. .44055))
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Lvvqepncayylsesnimmaplgwgwgiacilfigaaswyanwillagihyidgqrfiry
RDLMgFvpgrkmyyitwflQfitlilGnwgFillggralkaiHaeFsssHsparlQWF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTQAEKVFGAFGAIAAILVONTSGLLPEIQSTLRKPVVSNMRRALLLQYTAGAAVYYG
ISVACYWAYGAAVSEYLPDQLSGPSWATVLINATAFLQSIVSQHLFTVPIHEALDTQM
QRLDEGMFSRYNLGRRLLARGLVFGANAFVTALFPFWGDFVNLFGSFVLFPLFFMFPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IAATGEVYEAFAYEVPTISAMRNWLATSAALTVAYDVALIVILIKDGKSNKQKDYNVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LDELTSKISTLNLERVRQIKSRLVAISGRVQKVRDELEHLLDDEMDMAEMYLTEKLTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ILORRILKKERDAAAGGGKVRRAVVIJRGVTDDAAAAFVRLLYAGSSGDEEIDEKSAA
OMIVIAHAYRNPWIKRRCEGAIGSRLTAESSVVDTWQLAALCDAPQLHLRCTRLLAKEF
KAVEKTEAWRFLQENDPWLELDILQRLHDADLRRRKWRRKRAEGGVYVELSBAMDCLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="WVKVATYFAMTFGAFLFWQSMDRVHVWIALHQDEKKERMEREQE
IKRWQAELMAQAKESES"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HICTEGCTEVGPVGRAPAAAPCPAYATACRGLQLLIRHFSRCHRTSCPRCQRMWQLLR
LHAALCDLPDGHCNTPLCMQFRRKEEEKAAARKAKARAGDDDKWGLLVKKVRVARAMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement join(26102. .26407,26766. .26901,27028. .27170,
27656. .27784.28154. .28402,28988. .29359))
/gene="P0456E05.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(26102 .26407,26766 .26901,27028 .27170, 27656 .27784,28154 .28402,28988 .29359))
                                                                                                                                                                                                                                                                                                                                                                                                                                    translation="MCEGVRAAGDAAAADVDVITSSGRRRIPAHSTVLASASPVLES"
                                                                                                                                                                                                                                 /note="contains EST AU070785(R10238)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(join(23558, .23638,24837, .24941))
/gene="P0456E05.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(join(23558, .23638,24837, .24941))
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/protein_id="BaB92607.1"
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                                                                                                                           jóin(18574. 18678,18821. 18984,20752.
22377. 22336.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="contains EST AU162265(E30874)
unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            magnesium transporter-like protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="P0456E05.5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="BAB92605.1"
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                                                                                                                                                                                                                                                                                                                                                                        /protein_id="BAB92604.1"
/db_xref="G1:20804925"
                                                                   22377. .22536)
/gene="P0456E05.3"
                                                                                                                                                                                                                                                                                                               unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SLGKRRQMSCSQC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene
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                                                                                                             Clone: P0456E05

Published Only in Database (2001)

Sasaki. "." Matsumoto, T. and Yamamoto, K.

Sasaki." "MAR-2001) Takuji Sasaki, National Institute of
Direct Submission

May Sasaki." "Sciences" Rice Genome Research Program: Kannondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan
R=181-298-389-1486]

On May 15, 2002 this sequence version replaced gi:18181981.

Genes were predicted from the integrated results of the following:
Genes were predicted from the integrated results of the following:
Genes were predicted from the integrated results of the following:
Genes were predicted from the integrated results of the following:
Genes were predicted from the integrated results of the following:
Genes were predicted from the integrated results of the following:
GENSCANI. O. BLASTNZ. O. as well as SplicePredictor
(October 1998 version). The genomic sequence was searched against
NCBI NonRedundant Protein database, nr
(ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA sequence database at
RGP. Protein homologies of the coding regions were searched against
the identified cDNA sequences using BLASTNZ. O. with the
corresponding DDBJ accession no. and RGP clone ID.
A gene with identity or significant homology to a protein is
classified based on the protein name to indicate the homology covering
significant homology to any protein but with EST homology (covering
slagificant homology to any protein and T7 to SPG of the PAC clone.
This sequence of P0456E05 clone has an overlap with P0470Al2 (DDBJ:
This sequence of P0456E05 clone has an overlap with P0470Al2 (DDBJ:
AP003436) at the position 130,058 to 173,699 of 3' end Detailed
annotation of this entry is available at
information of this entry is available at
the price of P045E05 clone has an overlap with the
information of this entry is available at
the position 200,090 the position 200,090 the position 200,090 the position 200,090 the position 200,090 the position 200,090 the position 200,090 the position 200,090 the position 200,090 the position 200,090 the position 200,090 the positi
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EADSFPCFMELLSGFRDNFCQKLDNSAVGIQGTLSKLSQLVAKYDGELQRYLEITTEI
NPQFYAFRWITLLLTQEFNFADTIHIMDTLLSDPDGPQGRSIYRDGTGESMYTNIETS
VAHAYQSSRNSAVPVVEKLHRCRKATGAARLQFAAAPFLSPFRSPETTENAEAFPPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="Babg2602.1"
/db_xref="GI:20804923"
/translation="MCCLMPISTCACVCVERQQTQNADWLATPPAPAPAAAFALYYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VILNESCEDONCYAHARWANASIIIN"

complement(join(11701. 11960,11998. 12076,12765. 12881,
13131. 13310,13459. 13589,13660. 13758,14527. 14631,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(11701. .11960,11998. .12076,12765. .12881, 13131. .13310,13459. .13587,13660. .13758,14527. .14631, 15002. .15131,15421. .15487,17632. .17717,17924. .17952))
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WKLLLGYLPSDRALWEQELAKKRSQYAAFKEEFLSNPYSEIIEQIDRDYKRTHEDMHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MHEPLYRVHKKQQPVTAQHRPRLRGEATTLGSIRGRRRGSPHET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="P0456E05.2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .173699
/organism="Oryza sativa (japonica cultivar-group)"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
Sasaki,T., Matsumoto,T. and Yamamoto,K.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0456E05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similar to rabGAP domains protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         join(9483. .9641,10723. .10785)
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join(9483. .9641,10723. .10785)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="BAB92603.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="P0456E05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /chromosome="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene
                                                                                                                                                                     REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene
                                      AUTHORS
TITLE
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                                                                                                                                             JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMMENT
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Publication of the state of the
                      Oryza sativa (japonica cultivar-group) chromosome 1 clone P0456E05, ***, SEQUENCING IN PROGRESS ***, 3 ordered pieces. AC091071. GI:13450004
HTG. HTGS_PHASE2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16271
                                                                                                                                                                            Oryza sativa (japonica cultivar-group).
Oryza sativa (japonica cultivar-group).
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridaplantes; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaee; Oryza,
1 (basea; 1 to 174218)
Lee, J.-S., Hahn, J.-H., Yoon, U.-H., Lee, M.-C., Yun, D.-W., Kim, H.-I., and Eun, M.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 **NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and the accession number will be preserved.

* 53114 53213: contig of 53113 bp in length

* 53214 172404: contig of 53119 bp in length

* 172505 172504: gap of unknown length

* 172505 174218: contig of 1714 bp in length

* 172505 174218: contig of 1714 bp in length

* 172505 174218: "Apponbare"

//wariety="Nipponbare"
//db_aref="taxon:39947"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76 CACACCAAGCGTCGGCACCAATGGCTTACTACCAGGAGGTGGACTACTGCTCGGAGGAGG
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Unpublished
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Pred. No. 5.4e-17;
0; Mismatches 84;
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a 38377 c 37185 g 49417 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 30.4%;
Best Local Similarity 72.8%;
Matches 257; Conservative (
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/codon_start=1
/codon_start=1
/codon_start=1
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/db_xref="61:20804930"."
/db_xref="61:20804930"."
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/translation="WAASRLARENESERLEEVLYERPEOFIDSIRACELLEPF
SUSPARREDPHALDALASLREAADSFLEEVLEEVLERPEOFIDSIRACELLEPF
RAALLAFAASGDIPAASLASLREAADSFLPARENILLEVLYERPEOFIDSIRACELLEPF
RAALLAFAASGDIPAASLASLREAADSFLPAEFVNI ILHALARLRRHEDTVRFGE
RYSTRYREDVYFRILIASSCRAEGVDAANRWFGERRRWSCSPTGVSFNILMRGFFR
EGRCKEGIKVAREMLQLGFGLSVASMEININGLGKGGGEPKRAAEFFETELLVGVVPEG
FOLLDLVESLCRYRNVEKAVEVVELILERRWYSCLGVPAGVTVLECLMKEGKLDKACG
FORGIRKEGRAVLDEMLDAGTVPNIATTYNRLLDGLHMGREMQLQKCSHIRNAAN"
/GGON="PO456605.9"
/GGON="PO456605.9"
/GGON="PO456605.9"
/GGON="P0456605.9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(40277. .40417,40717. .40773,40875. .41073,
41173. .41300,41399. .41504,41677. .41756,42145. .42242,
42324. .42477. .42523. .42663,42757. .42841,43717. .44055))
/gene="po456E0557"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    253 ACCACCATGGTCACCACGGCGGCCACGGCTTCGTGGTGCGGAGACCAGGGTCGAAGAGG 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 8; Length 173699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches 84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-"hypothetical protein
similar to salt-inducible protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 174.6; DB (
Pred. No. 5.4e-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51367, ..52887
/gene="P0456E05.8"
51367, .52887
/gene="P0456E05.8"
                                                                                                                                                                   unknown protein"
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72.88;
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Best Local Similarity 72.8°
Matches 257; Conservative
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Birect Submission

All Sasaki.T., Matsumoto,T. and Yamamoto,K.

Direct Submission

Aporbiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan

(E-mail:tsasakiénias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Patis1-298-38-7468)

Tatis1-298-38-7441, Fars:18-298-38-7468)

On Oct 17, 2001 this sequence version replaced gi:1343001.

Genes were predicted from the integrated results of the following: GENSCANI, O, BLASTNA.O, BLASTNA.O, as well as SplicePredictor (October 1998 version). The genomic sequence was searched against (October 1998 version). The genomic sequence was searched against NCBI NonRedundant Protein database, nr (ftp://ncbi.nlm.nih.gov/blast/db) and the CDNA sequence database at RGP. Protein homologies of the coding regions were searched against NCBI NonRedundant Protein database with BLASTPS.O. ESTS represent the identified cDNA sequences using BLASTPS.O. With the corresponding DDDJ accession no. and RGP chone ID.

A gene with identity or significant homology to a protein name to indicate the homology level such as same name, 'putative' and 'like protein. A gene without significant homology to any protein but with EST homology (covering almost the entire length of partial sequence) is classified as an 'hypothetical' protein.

The orientation of the sequence is from SP6 to 77 of the PAC clone. The partial and information on one and assembly cnality tocether with next all and information on one and assembly cnality tocether with and assembly cnality and assembly cnality and assembly consistent workers.
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12046 ..12129,12315 ..12430,12535 ..12636,12715 ..12828,
12916 ..12972,13222 ..13288,13356 ..13409,13798 ..13872,
13956 ..13991,44389 ..14490)
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12046. .12129,12315. .12430,12535. .12636,12715. .12828,
12916. .12972,13222. .13288,13356. .13409,13798. .13872,
13956. .13991,14389. .14490)
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Location/Qualifiers
1. 185095
                                                                                                                                                                                       APUUJ436 185095 bp DNA linear PLN 17-APR-2002
Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1,
PAC clone:P0470Al2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza
                                                                                                                                                                                                                                                                                                                                                                                                   Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA,
clone:P0470A12.
                          /organism="Oryza sativa (japonica cultivar-group)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sasaki,T., Matsumoto,T. and Yamamoto,K.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0470A12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similar to Oryza satīva chromosome 5, P0574H01.5"
Published Only in Database (2001)
2 (bases 1 to 185095)
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/db_xref="taxon:39947"
/chromosome="1"
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                                                                                                                                                                      RESULT 3
AP003436/c
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KEYWORDS
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/translation="MAQYYSEVDHCAEEMNRPPHAGGEHYAVRRESYEEVDEMARAGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEMSYHEDNAVOKMSSSFREEKYYEQQGGAGGDVQVCRNGGAAAGAVQKHTYEEKKEEE
VYEESNHGGGGGGGCGGYARQHGAGGGQKHATYQHEVIKGYESAGGGYAAARINGGAGA
GVKROYSYREEEETDAGGYARINGGGVYOKOYSSR RRDEEEECDAAGGGYGRHHGAGG
GVKROYSYRORDEEETDAGGYARINGGOGGYNYNRHQDAVAGGGGHHYGGATAAAYGHGAGG
HFTAAAAGHHSSGGATOYHHQSYECEEEDSDEDDDCEDDDDDESDDDDGHCPPSRQC
SVHSYHQAAYQHEEKQHAGGRNHYHAVERHEFHGGGAQRYKOKYESSTQVGYAGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPASPPRGGRREAGGEGSGGGGRAPVINVTTRRSKRWRDSSGGRRDHAASRHDSIHT
RERTINWIGAIKLRPTFVGTREFRCCKPSLVVTPIWAGILGCHLCVLARLLCLRQQRWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RHAARHAVRNEALGYVVVLEHYPSPYAATMTRRKQQCATGAALPRYEAHTIENTTIGE
GEBERDYRQPPQGGLRTLRLHQQPRRYESTSCARIGGGSRAGEKHPTLNCQHQRHDRT
TDDQATVRNTTLKRKTTCMSYCHGRYQVWVQAPYQG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MARRRVGGGTSEVGGGNGEARGRRRQRSGRREARGARRLPRRG
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                                                                                                                                            DEDLSVQHFNAEAYIKLVRKHGLEISOPGLEPDKGLTWQMTKRLGDOEVHKVTEERPG
WCTDPHLPPCAAFVELMATYFSRDAWRCVWHMIQNDLVHGWGLDFALRRCVEPAHEKI
GVVDSQWVIHQVIPSLGNQGTAENGRTPWEGVRARCRKEWGMFQKRLADAEKAYYLGK
GITPPN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="BaB90277.1"
/db_xrefn="G1:20161353"
/translation="MAMARRGNGGYQYGAYSYGYGYSKPQVNYHSQSSESVTTVVTKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(join(19564. 19724,21382. 21688,22059. .22217,
22387. .22505.22923. .23035,23239. .23318))
/gene="P0470A12.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(join(27239. .27499,30542. .30622,30720. .30899,
                                                                                       KGAEGLAPGIVVPETDLYLRRLWGEPSEDLTSQPRYLITFTVGYSQKANIDAAVKKFS
                                                                                                                     ENFTIMLFHYDGRINDWDEFEWSKRAIHVSVRRQTKWWYAKRFLHPDIVAPYDYIFIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .21688,22059. .22217,
/protein_id="BAB90276.1"
| Dax xref="Gg1:20161352"
| Atranslation="MaKLAIIGRSSGIPRSNEGMRLLFSAVIGVMLGYLFGISFPTVN
| YTKLHFPSSIISYIEDKDSGITTQTLINHAWTSANSKKRNNSESNSDFFPRIYYDTNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(join(34470. .34734,34836. .34921,35025. .3511
35201. .35364,35440. .35601,35682. .35861,35978. .36414,
36513. .36568))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(join(19564 ..19724,21382 .21688 22387 ..25505,22923 .23035,23239 ..23318)) /gene="P0470A12.3"
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/gene="contains EST AU070442(S15668)
unknown protein"
                                                                                                                                                                                                                                                                                                                                                               /note="contains EST AU069076(C51993)
unknown protein"
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/gene="P0470A12.4"
complement (23929. .24237)
/gene="P0470A12.4"
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/db_xref="GI:20161355"
                                                                                                                                                                                                                                                                                                                      complement(15118. .16344)
/gene="P0470A12.2"
                                                                                                                                                                                                                                                                    complement(15118. .16344)
/qene="P0470A12.2"
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/gene="P0470A12.5"
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and Bur, M. Y.

Oryza sutiva PAC P0470A12 genomic sequence
Unpublished

1 Chases I to 185481)

E Abases I to 185481)

RS Barer to 185481)

RS Direct Submission

AL Submitted (29-MAR-2001) Rice Genome Sequencing Project, National Institute of Agricultural Science and Technology(NIAST), RDA, 249

Seodun-dong, Suwon 41-707, Korea (E-mail:)thahm@rda.go.kr,
Tel:182-131-290-0309, Fax:82-31-290-0308)

* NOTE: This is a "working draft' sequence. It currently

consists of 4 contigs. Gaps between the contigs

are represented as runs of N. The order of the pieces

are represented as runs of N. The order of the pieces

to the gaps between them are based on estimates that have

provided by the submittor.

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                                                                                                   27414 TCGTCAAGAAGATCCAGAGATCGACA-------GGTCCGGCTCCGGCCGCCACC 27364
                                                                                                                                                                                                                                          Oryza sativa (japonica cultivar-group) chromosome 1 clone P0470A12, *** SEQUENCING IN PROGRESS ***, 4 ordered pieces. AC091088 TG::13487944
                                                                                                                                                                                                                                                                                                                                   HTG: HTGS_PHASE2.

Oryza sativa (japonica cultivar-group).

Oryza sativa (japonica cultivar-group).

Oryza sativa (japonica cultivar-group)

Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta: Magnollophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

1 (basea: 1 to 185481)

Lee, J. - S., Hahn, J. - H., Yoon, U. - H., Lee, M. - C., Yun, D. - W., Kim, H. - I.
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                                                               193 TCGTCAAGGAGAAGTTCGAGGAGGTCGACGGTCTCACGCGGCGGCGGCGAACCACCACC
                                                                                                                                                                                               253 ACCACCATGGTCACCACGGCGGCCACGGCTTCGTGGTGCGGGGAGACCAGGGTCGAAGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   373 ACTGAGCCGCCGGCGGCCGGCATCCACGCCCGTTCGTGCTTGCCTGCGTGCC 425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41522 c 41493 g 50653 t
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Best Local Similarity 72.8
Matches 257; Conservative
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SOURCE
ORGANISM
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REFERENCE
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AC091088
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complement(join(34470. 34734,34836. 34921,35025. 35117,
35201. 35364,35440. 35601,35682. 35861,35978. 36414,
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                                                                                               36513. .36568))
/gene="p0470A12.6"
/note="contains ESTS AU058030(C61369),AU088621(C61369)"
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/note="contains ESTs
D15893(C1477),C72138(E1066),AU101125(E1066)
similar to Arabidopsis thaliana chromosome 4, F7J7_90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84; Indels 12; Gaps
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/product="putative RNA helicase"
/protein_id="BAB90381.1"
/db_xref="GI:20161357"
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                                                                                                                                        AAGAGGACATCAACCTGCACCGGCGAGGTCCACGAGGCGAGGGAGAGCTTCCTCGCCA 366
                                                                                                                                                       GGGCTAACTGAGCCGCCCGGCCGGCGATCCACGCCCGTTCGTGCTTGCCTGCGTGCCT 426
                                                                                                                                                                                                                        344 GGGCTGACTGAGCTTCGTGCTCCTGCTGCTCGTTTCGTATGTAACCTGTGTAAGG 403
                                                                                                                                                                                                                                                    427 TAIGTAIGTCIGTGGTIGACTGGTIGI ----TCAGGGTCATCGTACTTGGCTATCGTAC 481
                                                                                                                                                                                                                                                                  GTGCACGCACTCAGCTCCTGTACGAATTACGACAATAAGCTCGTGACCTG----AATAAA 537
                                                                                254 -----CCACCAIGGICACCACGGCGGCCACGGCIICGIGGIGCGCGAGACCAGGGICG 306
106 CGAIGGCCAAACCGGGCTTCGGCCGCCACGGCGGCGGCGTCCAGCAGTTCGTCGTCA 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     103 ACTACCAGGAGGIGGACTACIGCICGGAGGAGGIGAGGICGGIGGCCCCGGCCGGCTICG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163 GCCGCCACGGCGGCGGCGTCCAGCACGTCGTCAAGGAGAAGTTCGAGGAGGTCGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            223 CGGTCTCACGCGCCCGACCACCACCACCACCATGGTCACCACGGCGGCCACGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               283 TCGTGGTGCGCGAGACCAGGGTCGAAGAGGACATCAACACCTGCACCGGCGAGGTCCACG
                                                                                                                                                                                                                                                                                                                          226 GCCACCGCGGCAAACCAAGGCCACGCCACTTCCAGGCGCGCGAACAAGTTTG
                                            199 AGGAGAAGTTCGAGGAGGTCGACGGTCTCACGCGCCGGCGCCCAACCACCACCA----
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Gold, L., Tuerk, C., Pribnow, D. and Smith, J. Drew.
Systematic polypeptide evolution by reverse translation
Patent: US 6194550-A 7 27-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 390;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                  538 ACTICITCGIAATACTAAAAAAAAAAAAAAAAAAAAA 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches 129;
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                                                                                                                                                                                                                                                                                                                                                                                  DNA
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Pred. No. 4.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  390 bp
s 6194550.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="unknown"
126 c 133 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7 from patent US ARI35147 GI:14124052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.9%;
52.0%;
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Best Local Similarity
Matches 140; Conserv
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AR135147
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                         /product-"putative glycine-rich protein"
/product-"putative glycine-rich protein"
/protein_id-"CaB61838.1"
/db_xref-"G1:6478144"
/tb_xref-"G1:6478144"
/translation="MAHFKEWUDYEEVTSMAKPGFGRHGGGGVQQFVVKETFEEVEQV
/translation="MAHFKEWUDAETKFERHQHAHRRVPRAQGERPCQG"
1 154 g 112 t
                                                                                                                                                                                                                                                                                                                                                                  Sporobolus stapfianus mRNA for putative glycine-rich protein. AJ242802. GI:6478143
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                                                                                                                          252
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                                                                                                                                                                                                                                    ACAICAACACCIGCACCGGCGAGGICCACGAGCGCAGGGAGAGCIICCICGCCAGGGCIA 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 562)
Neale, A.D., Blomstedt, C.K., Bronson, P., Le, T.N., Guthridge, K.,
Evans, J., Gaff, D.F. and Hamill, J.D.
The isolation of lowly-transcribed genes which are induced during dessication of the resurrection grass Sporobolus stapfianus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (27-MAY-1999) Neale A.D., Biological Sciences, Monash
University, Wellington Rd Clayton, Victoria, 3168, AUSTRALIA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCAAGCGTCGGCACCAATGGCTTACTACCAGGAGGTGGACTACTGCTCGGAGGAGGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCGTCAAGGAGAAGTTCGAGGAGGTCGACGACGTCTCACGCGCGGGGGGCGAACCACCACC
                                                                                                                                                                                ACCACCATGGTCACCACGGCGGCCACGGCTTCGTGGTGCGCGAGACCAGGGTCGAAGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
             CACACCAAGCGTCGGCACCAATGGCTTACTACCAGGAGGTGGACTACTGCTCGGAGGAGG
                                                                  TGAGGTCGGTGGCCC---CGGCCGGCTTCGGCCGCCACGGCGGCGCGTCCAGCACG
                                                                                  373 ACTGAGCCGCCGGCGGCCGGCATCCACGCCCGTTCGTGCTTGCCTGCGTGCC 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sporobolus stapfianus.
Sporobolus stapfianus.
Sporobolus stapfianus
Sporobolus stapfianus
Sporobolus stapfianus
Sporobolus iviidiplantae; Streptophyta; Embryophyta; Trache
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae,
clade; Chloridoideae; Eragrostideae; Sporobolus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 562;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 143.8; DB 8;
Pred. No. 4e-12;
0; Mismatches 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Sporobolus stapfianus"
/db_xref="taxon:56623"
/clone="SDG137c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25.1%;
62.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  glycine-rich protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neale, A.D.
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321;
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                   92
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SST242802
LOCUS
DEFINITION
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222 228 282 288

RESULT

TITLE

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Complement(551. .3229)
/gene="SC3A7.02c"
/gene="SC3A7.02c"
/gene="SC3A7.02c, probable transcritional regulator, len:
892 aa; similar to e.g. MALT_ECOLI MalT regulatory protein
(901 aa), fasta scores; opt: 540 z-score: 495.9 E():
2.3e-20, 26.2% identity in 936 aa overlap. Contains
PSO017 APP /GTP-binding site motif A (P-loop).
helix-turn-helix motif from aa 848 to 686 (Score 1229,
43.37 SD) and Pfam match to entry PF00196 GerE, Bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / LTAIN LALGOR - WORDSDGTGESPADTGTDPLGGBY LRTRFVLPSRPATFLERORLI
VHLNQALRSPLTVVNGAAGAGKTLLTADWAAGLRVPTAWLTYETGDHPGVFWAYVFE
SLRVCGARAGDPFGAPADPSGYGORLLASLAAELINLLDSPVLLVLDBYDRWTNPETAE
GLOLPEYAASALVUTRTEPLLPLHRYRASGELTFEVRGSELSFTTEEAGALLRIH
GLOLPEYAASALVUTRTRGWAAGLRLSALAARESTDPRRYLKEFEAHHSTVADFLLARU
LHPLFREILRAHLRERLPGVEPELHIRAARWLRSSGFLFETHGFAAGDPLLARYR
VDDLALGGLFGTRAHLSRLDGVEPELHLRAARWLRSSGFLFETHGAAGGDPLLAGAG
VDDLALGGLFGCLSDALAQLFAGGRGFBARSPASDLYTAQALARBDYAGLNRLRGA
RNHLSDAGGLFGCLSDALAQLFAGGRGFBARSPASDLYTAQALARBDYAGLNRLRGA
HPELSALLHHVGSARLWGRRDARAVLTRYAGAATAGELRGELDPLLDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGWLGRAERRALAAVSEAERRGLPRPPGAGLGRLVLAAVAVDROELGRARVILLDETAR
LPAREBIDPVETAGRALAVSEABRACLEDVGETDAARKAAEPAVSTAVVSPWAEGQAAVARSA
ACLADGRPDPATALGSVGGDDPVCAVEAGTORAGGRAABA
VSVGAALVRARLAGSGGTVAACRLVARALLDARREHLRRPFLQAGDWTEPLLATAPL
HDLAEGWLPSGRPPAHGEPVRRGADPAFLVPVELSGBERDVLRRLARWMSTEETAADL
YVSINTVKTHLKSAVRKLANNRRGDAVRRARDLGLL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tianslation-"MPPAEPVRIRVRRPRRYFFGTCPKASWTAVWWSDAVFEPALPGL
SPATAGENCRPVRGRRPPSGARRSASRWVRRRPPCGSPPCWAWTHRPGGRQPSGSPSD
GLPATAHTSRRCPPACAQSRRGRTRWKRPACSRRGMPVGDPEDPANSCLEPMPPVPRS
STSLSCACPASRKRSPEWAABIAFLACPRAGLEALPVRMPGRLPGAILVPAAGRRLPR
FPGSRQILRPTTVARAFSPPGGGVTMRCWSACSGVSVILSFVGAKVGALRTLGPDVPFL
HGLAVKTRLAVSKRRFRPEYADGPGSWA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(3235, .4149)
/gene="SC3A7.03c"
/note="SC3A7.03c, questionable ORF, len: 304 aa; this ORF is not predicted as coding by positional base preference"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-"Pfam match to entry PF00196 GerE, Bacterial regulatory proteins, luxR family, score 50.40, E-value
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene-"SC3A7.02c", 3052)
/gene-"PS00017 AFP/GTP-binding site motif A (P-loop)"
/note-"PS00017 AFP/GTP-binding site motif A (P-loop)"
/note-"possible RBS upstream of SC3A7.02c"
/gene-"SC3A7.03c"
/note-"SC3A7.03c"

    103
/note="overlap with cosmid 3A7 from 1 to 102"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /transl_table=11
/product="putative transcriptional regulator"
/protein_id="CAA20065.1"
/db_xref="GI:3367740"
/db_xref="SPTREMBL:086603"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="very hypothetical protein SC3A7.03c"
/protein.id="CAA20066.1"
| Dexref="G1:3367741"
                                                                                                                                                                 complement(211. .217)
/note="possible RBS upstream of SC3A7.01c"
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                                     'db_xref="taxon:100226"
'clone="cosmid 3A7"
                                                                                                                                                                                                                            /gene="SC3A7.02c"
/note="scaA7.02c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(554. .745)
/gene="SC3A7.02c"
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                                                                                                                                                              complement(211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
                                                                                                misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic of Bibb et al., Gene 30:157-66(1984) and the FramePlot program http://www.nih.go.jp/
jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation
                                                                                                                                                                               BCT 12-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Parkhill, J., Barrell, B.G. and Rajandream, M.A.
Direct Submission
Submitted (30-JUL-1998) Streptomyces coelicolor sequencing project,
Sanger Centre, Wellcome Trust Genome Campus, Hinkron, Cambridge
CB10 ISA E-mail: barrellesanger.ac.uk Cosmids supplied by Prof.
David A. Hopwood, [3] John Innes Centre, Norwich Research Park,
Colney, Norwich, Norfolk NR4 7UH, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             correct initiation codon. Where possible we choose an initiation codon (atg) qtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions. Cosmid 3A7 lies between 10H5 and 4A2 on the Asel-B genomic restriction fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
1 (bases 1 to 35100)
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Notes:
Streptomyces coelicolor sequencing at The Sanger Centre is funded betails of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.

(URL; http://www.sanger.ac.uk/Projects/S_coelicolor/, CDS are numbered using the following system eg SC787.01c. SC (S. coelicolor), 787 (cosmid name), .01 (first CDS), c (complementary)
                                                                                                                                                                                                                                                       AL031155.2 GI:20520754
3-0xoadipate enol-lactone hydrolasse/4-carboxymuconolactone
decarboxylass, ABC transporter; beta-galactosidass; exonucleass;
IS3 type transposass; secreted amidass; secreted chitinass;
two-component sensor/regulator
Streptomyces coelicolor A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kinashi, H. and Hopwood, D.A.
A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome Mol. Microbiol. 21 (1), 77-96 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Redenbach, M., Kieser, H.M., Denapaite, D., Elchner, A., Cullum, J.,
                                                                                                                                                                               linear
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/strain="A3(2)"
                                                                                                                                                                               DNA
                                                                                                                                                                                             Streptomyces coelicolor cosmid 3A7. AL031155 AL645882
ACGACGACGACGACGCCCATGGTT 377
                                                                                                                                                                        35100 bp
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Oliver, K. and Harris, D.
Unpublished
3 (bases 1 to 35100)
                                                                                                                                                                                             DEFINITION
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COMMENT

FEATURES

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AC107225 150676 bp DNA linear HTG 17-JAN-2002 Oryza sativa chromosome 3 clone OSJNBa0026H19, *** SEQUENCING IN PROGRESS ***, 10 ordered pieces.
9889 TCGACGACTCCCCTGGAGCAACTGGACCAGGTGCTCCGCGCTGCGCACG 9948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukarota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryzeae; Oryzeae; Oryzeae; Oryzeae; U 150676)
Wing, R.A., Yu,Y., Soderlund, C., Chen, M., Kim, H.-R., Rambo, T., Saski, C., Henry, D., Oates, R. and Simmons, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E 2 (bases I to 150676)
Saski,C., Henry,D., Oates,R. and Simmons,J.
Saski,C., Henry,D., Oates,R. and Simmons,J.
Direct Submissation
Direct (17-JAN-2002) Clemson University Genomics Institute,
Clemson University, 100 Jordan Hall, Clemson, SC 29634, USA
ROTE: This is a "working draft, sequence. It currently
consists of 10 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces
are represented to be correct as given, however the sizes
of the gaps between them are based on estimates that have
                                                                                     283 TCGTGGTGCGCGAGACCAGGGTCGAAGAGGACATCAACACCTGCACCGGCGAGGTCCACG
                                                                                                                                                                                                  Chen, M., Kim, H. -R., Rambo, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      provided by the submillion.
This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.

1 11363: contig of 11363 bp in length
qap of unknown length
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contig of 3186 bp in length
app of unknown length
contig of 11960 bp in length
gap of unknown length
contig of 3201 bp in length
gap of unknown length
gap of unknown length
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1. 150676
/ Organism="Oryza sativa"
/db_xref="taxon:4530"
/chromosome="3"
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/gene="8C3A7.06c, probable transposase, len: 95 aa;
/note="8C3A7.06c, probable transposase, len: 95 aa;
/note="8C3A7.06c, probable transposase ORF's from many IS3 type insertion
similar to transposase ORF's from many IS3 type insertion
sequences of corynebacterium glutamicum TR:046069
(EMBL:X69104) IS3 related insertion element ORF! (97 aa),
fasta scores; opt: 244 z-score: 380.2 E(): 4.3s-14, 46.28
identity in 93 aad overlap. Contains probable colled-coil
from 55 to 93 and helix-turn-helix motif from aa 25-46
//coden absolute of the contains probable colled-coil
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NGDQLRWPPPHDNRCPRSQGRPSSVRAGGWPSFS"
complement (6207. .6494)
/gene="SC3A7.06c"
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ATPVPDLLQRGIAAOMPNTKNVGDITCLPVGNGQFLYLATVLDLCSKRLTGWSIADHM
PTSLVTDVLRAAARARGGGLRGAISHSGNGAQYVSKEFAQVCSELGVTRSRGAVGTS
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                                                                                                                                                                                                                                                                                                                                                                                        /translation="mlfysigmyiteaihsrelqypasawtpaaeydgeirdaawave
1TGDVQRYQRLAHSQGDGPARGLRPEPGRRGQRRGGAERSQQRSRSARPAEPSSTPAA
                                                                                                                                                                                                                                                                                                                                                                                                                                             GIPRVRGHÖPRRPPVRRHNGHOPVHLHNLPVHTGRPADPSHRPRRLPVDIRVRPVRPO
DQRGRPRQGPDPPVLRPTGPTHPDHRLPRHITPYDALNRITGTWAGSKTEANQLTAFT
                                                                                                                                                                    /note="SC3A7.04, questionable ORF, len: 384 aa; this ORF
is not predicted as coding by positional base preference"
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                                                                                                                                                                                                                                                                           /product-"hypothetical protein SC3A7.04"
/protein_id="CaA20067.1"
/db_xref="GI:3367742"
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Pred. No. 3.4;
0; Mismatches 151;
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/product="putative transposase"
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/protein_id="CAA20068.1"
/db_xref="G1:3367743"
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                                                                                                                                                                                                                                                                                                                                                                       db_xref="SPTREMBL:086605"
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                                                                                                                        1186. .5340
/gene="SC3A7.04"
                                                                                                                                                                                                                                                             _table=11
                                                             /gene="SC3A7.04"
/note="SC06336"
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                                                                                                                                                                                                                           55347 GGAGGTGTGTACCGCAAGGCGCAGATGGTCGACCCGGACGCCAACAAGGCCTGCAACCT 55288
                                                                                                                                                                                                                                                                                                      55168
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actII-1; actII-2; actII-3; actII-4; actIII; actIORF1; actIORF2; actII-1; actIV; actVA1; actVA2; actVA4; actVA5; actVA6; actVA6; actVA6; actVA7; actVA6; actVA7; actVA7; actVA6; actVB; actVII; bNA-binding protein; gntR-family regulatory protein; forein; merbyltcansferase; mini-circle protein; methyltcansferase; mini-circle protein; mutT-like protein; Streptomyces coelicolor protein; short-chain oxidoreductase. Streptomyces coelicolor A3(2).
                                                                                                                                                                                BCT 12-MAY-2002
                                                                                                                                                                                                                                                                                          229
                                                                                                                                                                                                                                                                                                                                                                                                                                                         290 GCGCGAGACCAGGGTCGAAGAGGACATCAACACCTGCACCGGCGAGGTCCACGAGGGCGAG 349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinopacteridae; Actinobacteridae; Actinobacteridae; Actinobacteridae; Streptomycetales; Streptomyces at 1 c 29080)

Redenbach, M., Kleser, H.M., Denapaite, D., Eichner, A., Cullum, J., Ridashi, H. and Hopwood, D.A.

A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome
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by the BBSRC and Beowulf Genomics
betails of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.

(URL, http://www.sanger.ac.uk/Projects/S_coelicolor/) CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                          170 CGGCGGCGCGTCCAGCAGCACGTCGTCAAGGAGAAGTTCGAGGAGGTCGACGGTCTC
                                                                                                                                                                                                                                                                                                                                                                  230 ACGCCCCGCCCAACCACCACCACCATGGTCACCACGGCGCCACGGCTTCGTGGT
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Cerdeno, A.M., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
Direct Submission
                                                                                                     Length 150676;
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                                 4 others
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                                                                                  Ouery Match 10.7%; Score 61.4; DB 2;
Best Local Similarity 51.3%; Pred. No. 2.8;
Matches 143; Conservative 0; Mismatches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptomyces coelicolor cosmid BAC28G1. ALS98942 AL645892
/clone="OSJNBa0026H19"
41031 a 35084 c 34425 g 40132 t
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Warren, T. and Harris, D.
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                   BASE COUNT
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LOCUS

The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the Framewellot program of Bibb et al., Gene 30:157-66(1984) as implemented at http://www.nih.go.jp/

Jun/Cgl-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Jif this cannot be identified we choose the most initiation codon. If this cannot be identified we choose the most upstream initiation codon. If this cannot be identified we choose the most initiation codon. If way be shorter because we arrange for a sequence overlapping sections once, or Ionger, because we arrange for a small overlap between neighbouring submissions. Cosmid StBAC28G1 note="nominal overlap with Streptomyces coelicolor cosmid /db\_xref="SPTREMBL:053903" /translation="MTANPGRPGGPADOGHPRRWAILGVLVLSLVGIILDNTVLNVTL RTLTDPEQGLGASHSQVEWVLSAYTLAFAATLFTWGVLGDRLGRRRVLLLGLGLFGLS LGIGEVTGGILLAHFWAGSVLLYNVPLAAGCLVAVVLVVPETRGTAGRRVDAGLLLS
IAGVVPLVYATIEAGRSGGYTRPAVWAAGLAGLGLLVFLWHERRTPEPSLELGFFRM
KASTAVAAVGFVSFAWAGFLFFSAFTLGSVRGYTPLGAGGCTVALAVANVCGPLST
VLVRSIGPRWVCAAGRAWGFLEFFSAFTLGSVRGYTPLGAGGCTVALAVANVCGPLST
VLVRSIGPRWVCAAGALGVALWGFTCGTFTTTTLYLFAALGAGVACWPTAAV
SIMNAIPREKAGVASAMNNTVRGLGGALGVAVLGSLMGAAYRGIEDELAVLPPSARH
OMGESLIDATLLAATRIGESGLVGPARQAFLDAMHLAAGAAAVALVGALAVLRWLPSS SLAGAYAĞSPEQLIAARACMGVSGAAVLPSTLATIAAVFPLRERPKALGIWAASVGFA /gene="SCBAC28G1.02"
//gene="SCBAC28G1.02, actVA1, probable integral membrane protein, len: 533 as, identical to previoualy sequenced TR:051903 (EMBL.X5883) Streptomyces coelicolor 6 ActVA region genes of the actinorhodin biosynthetic gene cluster, ActVA1, 533 as. Contains possible hydrophobic membrane spanning regions" /note="previously sequenced DNA fragment. EMBL:X58833.1 S.coelicolor 6 actVA region genes of the actinorhodin biosynthetic gene cluster" l. .73 'note="PS01162 Quinone oxidoreductase / zeta-crystallin :518 /note="previously sequenced DNA fragment. EMBL:X62373 S.coelicolor genes for hydroxyacyl-CoA dehydrogenase" /organism="Streptomyces coelicolor A3(2)" /transl\_table=11 /product="integral membrane protein" /protein id="CAG44189.1" /db\_xref="G1:14717083" VTTPTPPAGAVPGREHSDHLKVQGS' /strain="A3(2)" /db\_xref="taxon:100226" /gene="SCBAC28G1.02" /note="SCO5076; actVA1" /clone-"cosmid BAC28G1" Location/Qualifiers 2093. .2097 /gene="SCBAC28G1.02" 2105. .2500 484. .5883 /note="pre"

CDS

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"(bases 1 to 18420) The Cardeno, A. M., Parkhill, J., Barrell, B.G. and Rajandream, M.A. Direct Submission Submission Streptomyces coelicolor sequencing project, Submitted (14-APR-2000) Streptomyces
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                                                                              arenae hydrolase NcnH, 405 aa; fasta scores: opt: 1391 z-score: 1521.5 bits: 290.3 E(): 3.9e-77; 56.52% identity in 368 aa overlap" /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            348
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Streptomyces coelicolor A3(2).

Streptomyces coelicolor A3(2).

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

Actinomycetales; Streptomycineae; Streptomycescaceae; Streptomycescaceae; Itola420).

Redenbach, M., Kieser, H.M., Denapaite, D., Eichner, A., Cullum, J.,

Kinashi, H. and Hopwood, D.A.

A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome

Mol. Microbiol. 21 (1), 77-96 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGGAGGIGGACTACIGCICGGAGGAGGIGAGGICGGIGGCCCCGGCCGGCTICGGCCGCC 168
(EMBL:X58833) Streptomyces coelicolor 6 ActVa region gene of the actinorhodin biosynthetic gene cluster, ActVa5, 38 as and similar to TR:Q9F0J3 (EMBL:AF218066) Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         229 CACGCGCCGGCCCAACCACCACCACCATGGTCACCACGGCGGCCACGGCTTCGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            169 ACGCCGCCGCCGCCTCCACCACGTCGTCAAGGAGGTTCGAGGAGGTCGACACGGTCT
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0; Mismatches 153; Indels
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                                                                                                                                                                                                                                          /product="putative hydrolase"
/protein_id="CAC44193.1"
/db_xref="GI:14717087"
/db_xref="SPTREMBL:053907"
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Streptomyces coelicolor cosmid C30.
AL352972 AL645882
AL352972.2 GI:20520831
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Pred. No. 10
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nilarity 49.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KELRELGASIHTGDLEDAGSVRAAMKGAYGYFSIQTPMTPAGVEGEERQGKICADAAR
DLGYQHYVHSSYGGAERPEGVNWRLSKLAIEQRIQENALRFTFLRPSYFMENLNHDMS
PLVWEDGVLTFRRGLGPANTLQMISGPDIGYFRADAFDDPDTFGGARIELAGDELTGE
QIAAAFGRHTGLPARFYSYPIPELHRTGFEWQAISYTWLNGIGYHADIPTLRARFPQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        // gene="SCBAC28G1.04"
// gene="SCBAC28G1.04"
// forte="SCBAC28G1.04"
// forte
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RLSVRAEMGIRGFGILSRHPYEDVTEPPDABRLGGGGILSVDIESGILTFDFFLHSRLY
AVYERLALRPDAEFAAFTVOVPVADRTPGTLHRLEVGYDVAAGTAHWTADGOEVLSVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4346. :5491
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aa; identical to previously sequenced TR:053907
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131 aa; identical to previously sequenced TR:053904
(EMBL:X58833) Streptomyces coelicolor 6 ActVA region genes
of the actinorhodin biosynthetic gene cluster, ActVA2, 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="SCBAC28G1.05, actVA4, conserved hypothetical protein, len: 294 aa; identical to previously sequenced TR:053906 (EMBL:X58833) Streptomyces coelicolor 6 ActVA region genes of the actinorhodin biosynthetic gene cluster, ActVA4, 294 aa"
                                                                                                                                      protein, len:
TR:Q53904
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3465. .4349
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                                     /note="SC05077; actVA2"
2105. .2500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3465. .4349
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/qene="SCBAC28G1.06"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LTLDQWLARTGWTPRDPA'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . .3457
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gene

RBS

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COMMENT

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complement(1681.

complement(1681.

/gene="SCC30.02c"

/note="SCC30.02c, probable arac-family regulatory protein,

len: 278 aa; similar to SW:ARAc_SALY* (EMBL:J01797)

len: 278 aa; similar to SW:ARAc_SALY* (EMBL:J01797)

Salmonella typhimurium arabinose operon regulatory protein

Arac, 281 aa; fasta scores: opt: 232 -score: 270.4 E():

1.3e-07; 26.7% identity in 270 as overlap and to various

Streptomyces coelicolor putative arac-family

transcriptional regulators, e.g. TR:GO5480 (EMBL:AL031031)

S. coelicolor putative transcriptional regulator SC707.17

(SC4H8.01), 288 aa; fasta scores: opt: 638 z-score: 605.1

E(): 3.3e-28, 43.8% identity in 292 as overlap. Contains

Pfam match to entry PF00165 HHLArac, Bacterial regulatory

helix-turn-helix proteins, arac family and possible

helix-turn-helix motif at residues 189. .210 (+3.81 SD)"
                                                                                                                                                                                                                                                           /note="Pfam match to entry PF00892 DUF6, Integral membrane protein, score 38.50, E-value 1.6e-07" complement(1681. .2517)
                                                                                                                         entry PF00892 DUF6, Integral membrane E-value 1.9e-11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="SPTREMBL:09L019"
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VYGGLEVAYARGGHHISGPGSIVANLEDGEVHTGGPAAPEGSYSKRLTATAA
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RAADDTVPGAGRVARVVRDRLADELLAPPSLAALAADLGLSRYQLLARFRTSTGMPPY
WLAOHRVARARGLLDAGLBAPAALVGFADOAHLTRWFRRVLGVTPAAYRNSVQDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7628. .3389

/gene="SCC30.03" hypothetical protein, len: 253 aa;

/note="SCC30.03, hypothetical protein, len: 253 aa;

N-terminal region similar to TR:CAB52842 (EMBL:A109848)

Streptomyces coelicolor putative transcriptional regulator

SCI51.18, 548 aa; fasta scores: opt: 114 z-score: 134.1

E(): 5; 30.6% identity in 196 aa overlap. Contains

possible coiled-coil region at aprox residues 76. .93"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="Spremal.:091018"
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DPGHGLLRALYADFRAPAGAEAVRRAMEIAARGRRS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="SCC30.04, possible integral membrane protein, len: 204 aa; similar to TR:AAF12504 (EMBL:AE001863) Deinococcus radiodurans hypothetical 32.0 kD protein, 289 aa; fasta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(1699. .1956)
/gene="SCC30.02c"
/foote="Ffam match to entry PF00165 HTH_AraC, Bacterial
regulatory helix-turn-helix proteins, araC family, score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="hypothetical protein SCC30.03"
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                                                                                                      protein, score 51.40, E-val
                                                                                                                                                                                              complement(1212, .1622)
/qene="SCC30.01c"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
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/gene="SCC30.04"
                                                                                                                                                                                                                                                                                                                                                                                                            /note="SC02294"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="SC02296"
                                             misc_feature
                                                                                                                                                                                      misc_feature
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                                                                                                                                                                                                                                                                                                                                    gene
                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given prediction is based on positional base preference in codon. Gene specially developed Hadden Markow Model (Krogh et al., Nucleic Acids Research, 22(22):4769-4778(1994)) and the Frameplot program http://www.nih.go.jp/
Un/C91-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation ribosome binding site sequence (optimally 5-13bp before the most important initiation codon). If this equance (optimally 5-13bp before the most important initiation codon). If this commot be identified we choose the most important initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence everlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions. Cosmid C30 overlaps cosmid C75 on the Asel-C genomic restriction fragment.
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/gene="SCC30.01c"

/note="SCC30.01c"

26 as; similar to TR:BAA87714 (EMBI:AB016260)

#grobacterium tumefaciens TIORF89 protein, 306 as; fasta acores: opt: 396 a. soore: 465.4 E(): 1.88-18; 28.78

identity in 286 as overlap. Contains 2x Pfam match to entry PF00892 DUF6, integral membrane protein and possible hydrophobic membrane spanning regions"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="SPTRALS".95.
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CTAIAFVAFLELIKEVGPTRAGVITYVNPAVAVAAGALLLDEELTGGIGVAFTLIAG
SVLATAAAGFGREARRYPWSTRQTSRAGGRVESLITGLPEERPGSTGGGGG"
                                                                                                                                                                                                                                                                                      Details of S. Coelicolor sequencing at the Sanger Centre are available on the World Wide Web. (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/) CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 787 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                             Streptomyces coelicolor sequencing at The Sanger Centre is funded by the BBSRC and Beowulf Genomics
                          Campus, Hinxton, Cambridge
Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 ISA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 7UH, UK
On May 9, 2002 this sequence version replaced gi:7619747.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="probable ribonuclease P RNA, (rnpB) (positions taken from Streptomyces lividans EMBL:SLXLNB)" complement(681. .1661) /gene="SC0230.ulc" /note="SC02293"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="putative integral membrane protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .18420
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/strain="A3(2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:100226"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="cosmid C30"
complement(346. .771)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(346. .771)
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FEATURES

CDS

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TSPGRGGLLPAIRSRETAAHPEAVLOLROWGWSPPRGLAAGTADPYRWLALDERR
ALDGPAARPPRYGABLSGTEETYEALVAGLGCTCVATGNAFLITLGGVVTRPVRGLSF
SRYALARREDEGRALVRGYVEACRRVIDRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="putative methyltransferase"
/product="putative methyltransferase"
/product="dasobasis"."
/db_xref="ds:5541919"
/translation="MSTTDAVTFWDGVYAARPAPDAPRPNVRLVETVTGLPPGDALDL
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POEVAADLALDPATWRVERAEAPRRTATGFGGRTAEVVDHVLLVRRAD"
complement(1215. .1221)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="mpttprinrdppppprigggeaetlrgfldylrtslagkveddp
Epovrtaavasgtnilgilnhijhveravflgeevrswpatfraasgdgvadvvaryr
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                                                                 Direct Submission
Submitted (01-MAR-1999) F. Malpartida, Centro Nacional de
Biotecnologia, Microbiologia, Campus de la UAM 28049 Canto Blanco,
Madrid, 28049, SPAIN
Location/Qualifiers
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/protein_id="CAB51136.1"
                                                                                                                                                                                                                                                  coelicolor A3(2)"
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                                       Malpartida, F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6841 GCCCGGGTACTCGGCCACGTTGTTCGTCACGCCCGAGGTACTCGGCGGCCTCCACCAG 6900
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HVLDAAAGTLEVRACHTSPERTASVREERTTHTPADGELDLAVGSVTSVTV
LIGGPVAHLISFEGRREVRVVRCHADDPGAFVRAVELAREGHAVP"
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scores: opt: 178 z-score: 231.0 E(): 2e-05; 29.8% identity in 161 aa overlap. Contains possible hydrophobic membrane spanning regions"
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1 (bases 1 to 4851)

Wartinez.Costa, O.H., Martin-Triana, A.J., Martinez, E., Fernandez-Moreno, M.A. and Malpartida, F.

An additional regulatory gene for actinorhodin production in Streptomyces lividans involves a LysR-type transcriptional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /040. .4822
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/note="SCC30.05"
/note="SCC30.05"
/note="SCC30.05"
/similar to SW:YH13_CAMJE (EMBL:Z36940) Campylobacter
jejuni hypothetical 28.7 kD protein in HipO 3'region, 246
as, fasta scores: opt: 245 z'score: 295.9 E(): 4.9e-09;
28.1% identity in 210 aa overlap"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              249 CACCACCACCATGGTCACCACGGCGCCACGGCTTCGTGGTGCGCGAGACCAGGGTCGAA
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methyltransferase; mini-circle protein; oxidoreductase;
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99328982
10400594
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Pred. No. 13;
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Streptomyces coelicolor A3(2).
Streptomyces coelicolor A3(2)
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2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail:tsasAthaias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
Tel:81-298-38-7441, Fax.81-298-38-7468)

Tel:81-208-38-7441, Fax.81-298-38-7468)

On Mar 12, 2002 this sequence version replaced gi:16904696.
Genes were predicted from the integrated results of the following:
GENSCANI.0, BLASTNZ.0, BLASTNZ.0 as well as SplicePredictor
(October 1998 version). The genomic sequence was searched against
NCBI NonRedundant Protein database, nr
(ftp://ncbi.nlm.nh.gov/blast/db) and the CDNA sequence database at
NCBI NonRedundant Protein database, nr
(ftp://ncbi.nlm.nh.gov/blast/db) and the CDNA sequence database at
NCBI NonRedundant Protein database with BLASTPS.0. ESTS represent
corresponding DBDJ accession no. and RGP clone ID.
A gene with identity or significant homology to a protein is
corresponding DBDJ accession no. and RGP clone ID.
A gene with identity or significant homology to a protein
significant homology to any protein name to indicate the homology lovel
significant homology to any protein bact mane with a gene without
significant homology to any protein.
The orientation of the sequence is from Milzev to -21Mi3 of the BAC
Clone. This sequence of Bl147A04 clone has an overlap with P0431G06
(DDBJ: AP003683) clone at the position 141,300 to 142,270 of
P0431G06. Detailed information on overlap and assembly quality
together with annotation of this entry is available at
thetp://rgp.dna.affrc.go.jp/cenomeSeq.html.
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ADDQAPNGTDQDRTMWACSYPSRRRSMPGBNRMSSFAIDPLGIGDRSTOTTYRACOS
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/cultivar="Nipponbare"
/db_xref="taxon:39947"
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1278. .1520
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Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1,
AP003735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109 AGGAGGIGGACTACTGCTCGGAGGAGGIGGGTCGGTGGCCCCGGCCGGCTTCGGCCGCC 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             289 TGCGCGAGACCAGGGTCGAAGAGACATCAACACCTGCACCGGCGAGGTCCACGAGGGC
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae: Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoldeae; Oryzeae; Oryza.
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Clore:B1147a04
Published Only in Database (2001)
2 (bases 1 to 150053)
Sasaki,T., Matsumotco,T. and Yamamotco,K.
Direct Submission
Submitted (13-JUN-2001) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                169 ACGGGGGGGGGGTCCAGCAGGACGTCGAAGGAGAAGTTCGAGGAGGTCGACACGGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                229 CACGCGGCGGCGACCACCACCACCATGGTCACCACGGCGGCCACGGCTTCGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 4851;
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49.8%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                 1203. .4544
/gene="ORF12"
                                                                                                                                                                                                                                                                                                                                                  4203. .4544
/gene="ORF12"
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                                                                                                                                                                                                                1192. .4196
/note="ORF12"
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1777 C
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Best Local Similarity 49.8
Matches 144; Conservative
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AP003735
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54591 GAGGAGCTCCGCGGCGTCATGGTCGCCATCCTCGGCGGCGACGGCGACGGCTGCAGCCTC 54650
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54530
                                                                                                                                                                                                                                                                                    /translation="MSSGGVGGGSLGAGLLYHKFVSFALEETRLTTJTPHPSQEKFK
SIKPNDONTVFWALSFSAPKIRLLRSLTIEKKNSYQVLDFAAFSEPEYDLPIFCANVF
STHAGSIVVLDLNPLYDTTVHKDYKDKYRSIMPLYHKXNEWHLELMDOAIKENNKAT
ITHAGSIVVLDLNPLYDTTVHKDYKDKYRSIMPLYHKXNEWHLELMDOAIKENNKAT
IKRNQEGQHKYLTWRAEKDLVWEFLFEGVNTLGTKSFLDYFPEYARDGSVNKKRSMI
GKSFETRRWDANGETEGDAEAQ"
complement (62266. ..62823)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /prodes.ac.id="Bab86193.1"
/protesin_id="Bab8615"
/db_xref="G1:19386815"
/translation="MVKIKMPALFRRKSGSKSPPLPQADPASGGGSPAPTPEEMERV
FRKPANGDGRISKEEGALE-ESEGGRATDDELARMAABADADGDGFISLDEFAALNA
TASGDAAAVEEDLRHAFRVFDADGNGTISAAELARVLHGLGEKATVQQCRRMIEGVDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       248
                 ELDAVAAIAAEAEAGGGEDELMEAFKVFDADGDGRITAEELRGVMVAILGGDGDGCSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     309 GAGGACATCAACACCTGCACCGGCGAGGTCCACGAGCGCAGGGAGGTTCCTCGCCAGG 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
ISRSEASSFASASSESESSSDDALMARSTPRSVLPAEISRRELEAVLRRLGHGEPDDE
                                                                                                               complement(join(58262 .58450,58741. .58845,59228. .59321,59432 .55926,59957. .60076,60648. .60767))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      249 CACCACCACCATGGTCACCACGGCGGCCACGGCTTCGTGGTGCGCGAGACCAGGGTCGAA
                                                                                                                                                                                        //note="hypothetical protein
similar to Arabidopsis thaliana chromosome 3, F3L24.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129 GAGGAGGTGAGGTCGGTCGGCCCGGCTTCGGCCGCCACGGCGGCGCGCGTCCAGCAG
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                                                                                                                                                                                                                                                                                                                                                                                             complement (62266 . .62823)
/gene="B1147A04.10"
complement (62266 . .62823)
/gene="B1147A04.10"
/note="contains ESTS AU057966(S21949),(R10946)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.9%; Score 56.8; DB 8; Length 1 llarity 50.4%; Pred. No. 13; Conservative 0; Mismatches 137; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCTAACTGAGCCGCCGGCGGCGGCATCCACGCCC 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NGDGLISFEEFKVMMAGGGSFAKIA'
                                                                                                                                                                                                                                                     /protein_id="BAB86192.1"
/db_xref="GI:19386814"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unknown protein"
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Matches 139; Conserv
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AP004045/c
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/protein_id="mass6191.1"
/db_xref="GI:19386813"
/translation="MKLSIQSFARKLSLPSPKRTWSSGGGSSKRDGGMSKNGSGVKRA
                                                                                                                                                                                                                                                                                                                                                                                                                              VSGYRNEDKLAKLAMINDVVAARPODWTDNRPOCKENGSIRAKYPDFKNNVSKEALMIDTAP KAVLEKLIDDLVFSSDFSAAKKYRPFGGDKGNGELMQDLVDNPGKWWNNRSDKILFSVYF NRKGALFFRANLEQPESGAILSLEMGIDNPDVALSTYKCREDEDLCYYLLDAGFQCLIHI PADRCATILSFRANLEQFSTGILSLEMGIDNPDVALSTYKCREDLFYLLDAGFQCLIHI DGVFTRSTMINSLIMISISAMNOGYRLEFYNINSLIMISSLAMNOGYRLEFYNINSLEMSEPWYGRVLNRGATYMSYLMYBYSLRRI LSTAHVRRSTWMCMGAVASRHVQHRTFTSRTVARVRGACGMLELFVVSSSQCAVLIVL
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/db_xref="GI:19386812"
/translation="MRHLARLIANNRILLPASSSPAAAFSKRTYARRTKPAPPTADAAA
                                                                                                                                                                                                                                                                                                                                                                         PAAVEGEGEEERGPGWQREKLPAEIPRPSTIAFQPRVANAVRLVGTVGAPVQLQRLPD
GRFSAVSVLVQDRHADYPKFWIPIIFQDDLAQVAASHLQEKDHIYVSGQLTGDIPPTK
                                                                                                                                                                                                                                                                                                                                                                                                              LMDGQANIQVLAQMLSFVGGKAVQADSMVDEEEGFMQIVEAEKKVETKKFIPKYPPRT
                          complement(join(10608. 10810,11617. 11717,14329. 14407, 15809. 15855,16152. 16202,17629. 17645,17914. 17999, 1703. 18807,18902. 18965,19771. 19832,20405. 20567, 20648. 20751,22499. 22402,23005. 23143,23829. 24196))
                                                                                                                                                                                                                                          /note="hypothetical protein
similar to Arabidopsis thaliana chromosome 4, At4920010"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="3' LTR"
54171. .54785
/gene="B1147A04.8"
54171. .154785
/gene="B1147A04.8"
/note="contains_ESTS_AU057399(S21412),AU057400(S21412)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(44492. .45414)
/gene="Bl147A04.6"
complement(44492. .45414)
/gene="Bl147A04.6"
/note="probably inactive due to frameshift(s) in CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(36287. .43479)
/gene="Bl147804.7"
complement(35287. .43479)
/gene="Bl147A04.7"
/note="probably inactive due to frameshift(s) in CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="probably inactive due to frameshift(s) in CDS
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gene="B1147A04.6"
/note="probably inactive due to frameshift(s) in CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similar to Oryza sativa chromosome 1, P0492F05.19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similar to Oryza sativa chromosome 1, P0492F05.19"
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similar to Oryza sativa chromosome 1, P0684B02.19"
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/gene="B1147A04.6"
complement(32547. .34495)
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24705. 22574
.note=="5" LTR"
25762. 31913
/gene="B1147A04.5"
/gene="B1147A04.5"
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5417
                                                                                                                                                                                                                                                                                            /codon_start=1
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                                                                                            Sasaki, T., Matsumoto, R.

Direct Submission

AD Submitted (15-MG-2001) Takuji Sasaki, National Institute of
Agrobiological Resources, Rice Genome Research Program; Kannondai

2-1-2, Takubb, Ibaraki 305-8602, Japan

(2-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
Tel:81-298-38-7441, Fax:81-298-38-7468)

Tel:81-298-38-7441, Fax:81-298-38-7468)

Tel:81-298-38-7441, Fax:81-298-38-7468)

The nuclocitide sequence of this BAC clone was generated by
Combining Monsanto and RGP-Japan sequencing data.

NOTE: It currently consists of 1 contigs. Gaps between the combining Monsanto and RGP-Japan sequence of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* Location/Qualifiers

// Corganism="Oryza sativa (japonica cultivar-group)"

// AD xref="Laxon:qaq47"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38485 GCGGCGTCCTCCTGGACCACGCCACCGGGTGGTCATCGGCGAGACCGCCGTCGTCGCGG 38426
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138289 bp DNA linear HTG 31-MAY-2002
Oryza sativa (japonica cultivar-group) chromosome 2 clone P0453G09,
*** SEQUENCING IN PROGRESS ***, in ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     172 GCGGCGGCGTCCAGCAGCACGTCGTCAAGGAGAAGTTCGAGGAGGTCGACACGGTCTCAC 231
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38305 TCAGGATCGGCGGCGCGCGAGATCGGGGCCGGGTCGCTGGTGGTCGCTGGCGACGTGC 38249
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    Sasaki,T., Matsumoto,T. and Yamamoto,K.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2, BAC
clone:0J1135_F06
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Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2, PAC
clone:P0453G09
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Best Local Similarity 52.3%; Pred. No. 17;
Matches 124; Conservative 0; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="OJ1135_F06"
22012 c 21866 g 27986 t
                                                            Published Only in Database (2001)
2 (bases 1 to 102688)
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HTG; HTGS_PHASE2.
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14835 GEGGGGTCCTCCTGGACCACGCCACCGGGTGGTCATCGGCGAACCGCCGTCGTCGGCG 24894
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Bacteria: Firmicutes; Actinobacteria: Actinobacteridae;
Actinomycetales: Streptomycineae; Streptomycetaceae; Streptomycetales: Streptomycineae; Streptomycetales: Streptomycineae; Streptomyces.

(bases 1 to 3164)

(chases 1 to 1164)

(chases 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Oryza sativa (japonica cultivar-group)"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
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0; Mismatches 113;
                                                                  Sasaki,T., Matsumoto,T. and Yamamoto,K.
Direct Submission
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olished Only in Database (2002) (bases 1 to 138289)
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REFERENCE
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2 (bases 1 to 3164)

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BAPARLYFGISFPLFPDLGHYPDTEPVPRQDAPFVVGGVR
1236 c 1003 g 437 t 1 others
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(db_xref="AG1:8118603"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein_id="AAF73051.1"
| Debaref="AG1:811862"
| Arransiation="WHRLSPDAAYYTLVNVFTVSPDDQEKLYRHLVDVTERTIRHLPG
| SYSATFHLGNNGRHVVNYAOWESEETFRSMHALPELQEHFAFCRGIATPLSVPCAVAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KVVAAGYRYTSSAVLGAAVPTAIPHELALTGLPGORVPHVWLDHDGRRVSTVDLAVDG
FVILARADGTPWADAAARLAATTGIPLIAHYVGKTLTDPADALAAATGLGEAGALLLR
PDGFVAWRSDTSADDPEAVLDGVLARILART"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Translation="MDRIEIPVLVVGGGLTGLAAAVFLRQQGVDCLLVERHRSTTFLT"
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NLAWKLASVLHGRASDALLDTYHQERHPVGTEIAEQAWTRHTYRLDGDDELGRRLVDT
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Rafanan, E.R. Jr., Le, L., Zhao, L., Decker, H. and Shen, B.
Direct Submission
Submitted (03-MAY-2000) Chemistry, University of California
Davis, One Shields Ave., Davis, CA 95616, USA
Location/Qualifiers
1. 3164
/organism="Streptomyces olivaceus"
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/db_xref="taxon:47716"
339. .1958
/gene="elmG"
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2648. .3079
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1990. .2319
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'qene="elmI"
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Length 3164;

9.5%; Score 54.6; DB 1;

Query Match

487

BASE COUNT ORIGIN

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2495 gccdaagarccrcdaggcccgcgacgacgccccccc3754
                                                                                                 2434
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                                           293 CGAGACCAGGGTCGAAGAGACATCAACACCTGCACGGCGAGGTCCACGAGGCAGGGA 352
                            173 CGGCGGCGTCCAGCACGTCGTCAAGGAGAAGTTCGAGGAGGTCGACACGGTCTCACG
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Zea mays
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 417)
Hunter, B.G., Beatty, M., Singletary, G., Hamaker, B., Larkins, B.A. and
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Contact: Jung R
Trait and Technology Development, Food and Feed Research Pioneer Hi-Bred International, Inc.
7300 NW 62nd Ave., P.O. Box 1004, Johnston, IA 50131-1004, USA Fax: 515 270 5934
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10 AW787315
10 BE02533
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11 BE19299
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Location/Qualifiers
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Word size :

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Run on:

Database :

/organism="Zea mays" /db\_xref="taxon:4577"

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FEATURES

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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoldeae; Andropogoneae; Zea.
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/dev_stage="adult"
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/clone_lib="Pioneer AF-1 array"
//note="Vector: pSport1; Site_1: Sal1; Site_2: NotI"
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/cultivar="W23"
/b xref="taxon:4577"
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Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, US
Tel: 650 723 227
Fax: 650 725 8221
Fmail: Walbot@stanford.edu
Plate: 707009 row: E column: 07.
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500 bp mRNA linear EST 16-MAY-2000 adult tissues from Walbot lab, same as 707 sequence.
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1 (bases 1 to 500)
Walbot,V.
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/note="Organ: tassel, kernel, silk, husk, root, leaf; vector: pGAD10; Site_1: EcoRI; cDNa library from fully vector: pGAD10; Site_1: EcoRI; cDNa library from fully differentiated maize tissues from an active Mutator plant. Tissue ratio is 4/2/1/1/1/1 (tassel, kernel, silk, husk, root, leaf). Unidirectionally cloned."

a 170 c 157 g 89 t lothers
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Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
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                                                                                                           DB 10;
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/note="Organ: tassel, kernal, silk, husk, root, leaf;
Vector: pGAD10; Site_1: EcoRI; cDNA library from fully
differentiated maize tissues from an active Mutator plant.
Tissue ratio is 4:2:1:1:1:1 (tassel, kernel, silk, husk,
root, leaf). Unidirectionally cloned. New library number
given to library 707 for additional sequencing."
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 465)
Walbot, V.

Maize ESTs from various cDNA libraries sequenced at Stanford
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/clone_lib="945 - Mixed adult tissues from Walbot lab, same as 707 (SK)"
/tissue_type="tassel, kernal, silk, husk, root, leaf"/dev_stage="fully-grown"
/lab_host="bH108"
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                                                                                                                                                                                                                                                                                                                                                                                     Length 465;
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                                                         Maize bold
University
University
Contact: Walbot V
Contact: Walbot V
Department of Biological Sciences
Stanford University
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Fax: 650 723 227
Email: Walbotéstanford.edu
Email: Walbotéstanford.edu
Plate: 945032 row: C column: 12.
Location/Qualifiers
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99.6%; Pred. No. 0;
iive 0; Mismatches
        Eukaryota; Viridiplantae;
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BE129897 GI:857726A
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                                                                                                                                                                                                                                cch 67.4%; Score 387; DB sl Similarity 99.6%; Pred. No. 0; 487; Conservative 0; Mismatches
                         90
Fax: 650 725 522
Email: walbot@stanford.edu
Plate: 945002 row: E column:
Location/Qualiflers
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Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="tassel, kernel, silk, husk, root, leaf"
/dev_stage="adult"
/lab_host="bhl0b"
/note="organ: tassel, kernel, silk, husk, root, leaf;
/note="organ: tassel, kernel, cDNA library from fully
differentiated maize tissues from an active Mutator
plant. Tissue ratio is 4/2/1/1/1/1 (tassel, kernel, silk,
plant, root, leaf). Unidirectionally cloned."
a 158 c 149 g t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243 AACCACCACCACCATGGTCACCACGGCGCCCACGGCTTCGTGGTGCGCGAGACCAGG 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182 AACCACCACCACCACCACGACGACGACGACGACACGCTTCGTGGTGCGCGAGACCAGG 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 CGCIGCGCACAGACACACCAAGCGICGGCACCAATGGCITACTACCAGGAGGTGGACTAC 122
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707049E04.x1 707 - Mixed adult tissues from Walbot lab (SK) Zea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
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Walbot,V.
Maize ESTs from various cDNA libraries sequenced at Stanford
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                                                                                                                                                                                                                        Contact: Walbot V
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Plate: 707049 row: E column: 04.
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                                    Mays cDNA, mRNA sequence
AW331212
AW331212,1 GI:6827569
                                                                                                                                                                                                   University
Unpublished (1999)
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Zea mays
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552 bp mRNA linear EST 07-JUN-2000 945028B09.Y1 945 - Mixed adult tissues from Walbot lab, same as 707 (SK) Zea mays cDNA, mRNA sequence. BE025302 BE025302.1 GI:8318737 EST.
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Vector: pGADIO. Site_1: ECORI; cDNA library from fully
differentiated maize tissues from an active Mutator plant.
rissue ratio is 4:2:1:1:1:1 (tassel, kernel, silk, husk,
root, leaf). Unidirectionally cloned. New library number
given to library 707 for additional sequencing."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea. 1 (bases 1 to 552)
                                        362 GCCTTATGTATGTCTATGGTTGACTGGTTGTGCAGGGTCATCGTACTTGGCTATCGTACG 421
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/organism="Zea mays"
/organism="W23"
/db_xref="taxon:4577"
/db_xref="taxon:4577"
/db_xref="taxon:4577"
/clone_lib="945 - Mixed adult tissues from Walbot lab,
same as 707 (SK)"
/tissue_type="tassel, kernal, silk, husk, root, leaf"
/dev_stage="fully-grown"
/lab_host="DH10B"
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Unpublished (1999)
Contact: Walbot V
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Stanford University
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Email: Walbotdestanford.edu
Plate: 945028 row: B column: 09.
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945028B09,y2 945 - Mixed adult tis
(SK) Zea mays CDNA, mRNA sequence.
BE025303
BE025303.1 GI:8318738
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/organism="Zea mays"
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Vector: pGAD10; Site_1: EcoRI; cDNA library from fully
differentiated maize tissues from an active Mutator plant.
Tissue ratio is 4:2:1:1:1:1 (tassel, kernel, silk, husk,
root, leaf). Unidirectionally cloned. New library number
given to library 707 for additional sequencing."
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                                       469 TTGGCTATCGTACGTGCACGCACTCAGCTCCTGTACGAATTACGACAATAAGCTCGTGAC 528
                                                                                                                                                                                                                                                                                                                                                                                                                                        Spermatophyta; Tracheophyta; Embryophyta; Tracheophyta; Spermatophyta; Tracheophyta; Clade; Palcoldeae; Paccalade; Palcoldeae; Andropogoneae; Zea.

1 (bases 1 to 436)
Walbor v
                                                                                                         468
                                                                                                                                                             408
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/organism="Zea mays"
/coultivar="W33"
/db_xref="taxon:4577"
/clone_lib="%95 - Mixed adult tissues from Walbot lab, same as 707 (SK)"
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/dev_stage="fully-grown"
/lab_host="bully-grown"
/lab_host="bully-grown"
/lab_host="bully-grown"
/cone.libe_host="bully-grown"
349 GGGAGAGCTTCCTCGCCAGGGCTAACTGAGCCGCCGGCGGCGGCGGCATCCACGCCGGTTC
                                                                                                                                                GTGCTTGCCTGCGTGCCTTATGTATGTCTGTGGTTGACTGGTTGTTCAGGGTCATCGTAC
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Maize ESTs from various cDNA libraries sequenced at Stanford
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                                                                                                                                                                                                                                                     855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227
Fax: 650 728 8221
Exal: walbot@stanford.edu
Plate: 945002 row: E column: 06.
Location/Qualiflers
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iive 0; Mismatches
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Contact: Malbot V
Department of Biological Sciences
Stanford University
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AUTHORS
TITLE
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JOURNAL

COMMENT

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mRNA linear EST 07-JUN-2000 tissues from Walbot lab, same as 707
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Vector: pGAD10; Site_1: EcoRI; cDNA library from fully
differentiated maize tissues from an active Mutator plant.
Tissue ratio is 4:2:1:1:1:1 (tassel, kernel, silk, husk,
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Spermatophyta; Pagnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoleae; Andropogoneae; Zea.
1 (bases 1 to 326)
Walbot,V.
Maibot,V.
                                                          234
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                                                                                                                                        241 GCTTCCTCGCCAGGCCTAACTGAGCCGCCCGCGCGCGCCGCATCCACGCCCGTTCGTGCTT
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                                                          GCGGCGTCCAGCACGTCGTCAAGGAGAAGTTCGAGGAGGTCGACGGTCTCACGCG
                                                                              AGACCAGGGTCGAAGAGGACATCAACACCTGCACGGCGAGGTCCACGAGGGCAGGAGA
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University
Unpublished (1999)
Contact: Walbot (1999)
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 8221
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 945028 row: B column: 09.
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AW288875 .274 bp mRNA linear EST 16-JAN-2000 707009E07.x3 707 - Mixed adult tissues from Walbot lab (SK) Zea mays cDNA, mRNA sequence.
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1 (bases 1 to 274)
Walbot,V.
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/clone_lib="707 - Mixed adult tissues from Walbot lab (SK
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Vector: pGAD10; Site_1: EcoR1; cDNA library from fully
                                                                                                                                                                                                                                                                                                                                                                 223 CITCGTGGTGCGCGAGACCAGGGTCGAAGAGAACACATCAACACCTGCACCGGCGAGTTCCA
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/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                          Maize ESTs from various cDNA libraries sequenced at Stanford
Tissue ratio is 4:2:1:1:1:1 (tassel, kernel, silk, root, leaf). Unidirectionally cloned. New library given to library 707 for additional sequencing."

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855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 65725 8221
Email: walbot@stanford.edu
Plate: 707009 row: E column: 07.
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/cultivar="W23"
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Best Local Similarity 99.4%;
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Contact: Walbot V
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Vector: pGAD10; Site_1: EcoR1; cDNA library from fully
differentiated maize tissues from an active Mutator plant.
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/clone_lib="945 - Mixed adult tissues from Walbot lab, same as 707 (SK)"
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Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 227
Fax: 650 725 821
Email: walbot@stanford.edu
                                                                                                                                             DB 10;
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Pred. No. 0;
0; Mismatches
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Plate: 945027 row: E column: 06.
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Matches 304; Conservative
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Vector: pGAD10; Site_1: EcoR1; cDNA library from fully
Vector pGAD10; Site_1: EcoR1; cDNA library from fully
differentiated maize tissues from an active Mutator plant.
Tissue ratio is 4:2:1::1:1 (tassel, kernel, silk, husk,
root, leaf). Unidirectionally cloned. New library number
given to library 707 for additional sequencing."
                                                                                                                                                                                              160 TCGGCCGCCACGGCGCGCGCGTCCAGCACGTCGTCAAGGAGAAGTTCGAGGAGGTCG 219
                                                                                                                                                                                                                                                                     121 TCGGCCGCCACGGCGCGCGCGCCTCCACCACGTCCACGTCCACGTCCAGGAGAGAGTCCAGGAGGTCG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Zea.
differentiated maize tissues from an active Mutator
plant. Tissue ratio is 4/2/1/1/1/1 (tassel, kernel, silk,
husk, root, leaf). Unidirectionally cloned."
a 91 c 93 g 33 t
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                                                                                                                                        CAAGCACTTCGACGTCACAGGGCGCTGCGCACAGACACACAAGCGTCGGCACCAATGG
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/clone_llb="945 - Mixed adult tissues from Walbot lab,
same as 707 (SK)"
/tissue_type="tassel, kernal, silk, husk, root, leaf"
/dev_stage="fully-grown"
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                                                                                      DB 10; Length 274;
                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                        855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2237
Fax: 650 728 8221
Email: walbot@stanford.edu
Plate: 945007 row: B column: 05.
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                                                                                   38.9%; Score 223; DB
100.0%; Pred. No. 0;
:1ve 0; Mismatches
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Stanford University
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/organism="Zea mays"
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Maize ESTs from various
                                                                                               Best Local Similarity 100. Matches 223; Conservative
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Unpublished (1999)
Contact: Walbot v
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Zea mays
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Length 476;

10; BB

Score 210;

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Query Match

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/organism="Zea mays"
/db_xref="dbEST:945032C12.Y1"
/db_xref="taxon:4577"
/clone_lib="lob" - Unique I from Maize Genome Project"
/note="This library represents the unique ESTs found in
the first round of EST sequencing at Stanford University
for the maize genome project. Sequences are present from
libraries 486, 487, 496, 603, 605, 606, 614, 618, 660,
687, 707, and 945. Contigs were assembled using TIGR's
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( Dases 1 to 311)
Walbot, V.

Malbot, V.

Malse ESTs from various cDNA libraries sequenced at Stanford
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                                                                                                                                          218 CGACACGGTCTCACGCGGCGCCCAACCACCACCACCATGGTCACCACGGCGGCCA
                                                                                                                                                                                                                                                                278 CGCCTTCGTGCTGCGCGAGACCAGGGTCGAAGAGGACATCAACACCTGCACCGGCGAGGT
                    Gaps
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Pred. No. 0;
); Mismatches
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Department of Biological Sciences
Stanford University
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1000077C04.x2 1000 - Unigene I
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BF729420
BF729420.1 GI:12047
              Conservative
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Vector: pGAD10; Site_1: ECORI; cDNA library from fully
differentiated maize tissues from an active Mutator plant.
Issue ratio is 4:2:1:1:1:1 (tassel, kernel, silk, husk,
root, leaf). Unidirectionally cloned. New library number
given to library 707 for additional sequencing."
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 496)
                                                                                                                                                                                                                                                                                                                                                     422
   CAP program and a representative EST from each contig was selected for the Unigene set. All singlets were also selected." 107 g 46 t
                                                                                                                                                                              54 CAGCAGCACGTCGTCGAGGAGAAGTTCGAGGAGGTCGACACGGTCTCACGCGCCGCGGCGGCCGC 113
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                                                                                                                                                                                                                                                                                       GTCGAAGAGGACATCAACACCTGCACCGGCGAGGTCCACGAGCGCAGGGAGAGCTTCCTC 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Zea mays"
/cultivar="W23"
/db_xxref="taxon:4577"
/clone_lib="945 - Mixed adult tissues from Walbot lab,
same as 707 (SR)"
/tissue_type="tassel, kernal, silk, husk, root, leaf"
/dev_stage="fully-grown"
/lab_host="DH10B"
                                                                                                                                                                                                                       183 CAGCAGCACGTCGTCAAGGAGAAGTTCGAGGAGGTCGACACGGTCTCACGCGCCGGCGCC
                                                                                                                                Gaps
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                                                                                               Length 311;
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                                                                                               Score 207; DB 12; Length 3 Pred. No. 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
plate: 945002 row: E column: 06.
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945002E06.XI 945 - Mixed adult tis
(SK) Zea mays cDNA, mRNA sequence.
AW787314
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99.6%;
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Unpublished (1999)
                                                                                                                                  257; Conservative
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AW787314.
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BQ619167 EAT 27-JUN-2002 RNOSEQ4E05_SK.abl Salt stressed Zea mays roots cDNA library Zea mays cDNA clone RNOSEQ4E05_SK.abl similar to No homology, mRNA
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| Wang, H. and Bohnert, H.J. Genomics of plant stress tolerance Unpublished (2002)
| Contact: Mark Fredricksen Department of Plant Biology
| University of Illinois
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                                                              249 CACCACCACCATGGTCACCACGGCGGCCACGGCTTCGTGGTGCGGGGAGACCAGGGTCGAA 308
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/db_xref="taxon:457"
/db_xref="taxon:457"
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/clone=lib="Salt stressed Zea mays roots cDNA library"
/fissue_rype="Roots"
/dev_stage="Z weeks old"
/note="vector: pBluescript SK+; Stressed 24 hours at l
                                                                                                                               183 CACCACCACGAGGTCACCACGCCACGCTTCGTGGTGCGCGAGACCACGGGTCGAA
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Length 496;
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 DB 10;
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                                  0; Mismatches
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Tel: 2172655473
Email: bohnertlab@llife.uluc.edu.
Score 200;
Pred. No. 0
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99.1%;
Query Match 34.8%;
Best Local Similarity 99.3%;
Matches 300; Conservative
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Best Local Similarity 99.1
Matches 328; Conservative
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423
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACC
clade, Panicoldeae, Andropogoneae, 2ea.
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/note="Vector: pBluescript SK+; Stressed 24 hours at 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 364 CCAGGGCTAACTGAGCCGCCGGCGGCGATCCACGCCCGTTCGTGCTTGCCTGCGTG
                                                                                                                                                                                                                                                                                                                            CCTTATGTATGTCTGGTTGACTGGTTGTTCAGGGTCATCGTACTTGGCTATCGTACGT
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/clone="RNOSEO6CO6_SK.abl"
/clone="lb="Salt stressed Zea mays roots cDNA library"
/tlssue_Lype="Roots"
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Unpublished (2002)
Contact: Mark Fredricksen
Department of Plant Blology
University of Illinois
1201 W. Gregory Dr., Urbana, IL 61801, USA
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Homo sapiens
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Extaryota: Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3454)
Koehrer.K., Beyer,A., Mewes,H.W., Well,B. and Wlemann,S.
Direct Submission
Submitted (12-MAR-2002) MIPS, Am Klopferspitz 18a, D-82152

REFERENCE AUTHORS TITLE JOURNAL

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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120   17.8   1517   9   1517   1517   1517   9   1517   1517   9   1517   9   1517   9   1517   9   1517   9   1517   9   1517   9   1517   9   1517   9   1517   9   1517   9   1517   9   1517   9   15025121   14000 8a   120   17.8   1652   9   16025176   1602   17.8   1652   9   16025176   1602   17.8   1602   9   16025776   1602   17.8   1602   9   16025776   1602   17.8   1602   9   16025776   1602   17.8   1602   9   16025776   1602   17.8   1602   9   16025776   1602   17.8   1602   9   16025776   1602   17.8   1602   9   16025776   1602   17.8   1602   9   16020705   1602   17.8   1602   9   16020705   1602   17.8   1602   9   16020705   1602   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8	15	120	_		טע	BCO3Z46Z XI,NAKATD	OMC
120   17.8   1652 9   BC028121   BC028121   Homo Sa     120   17.8   1699 9   HSM801509   AL133659   AL133659     120   17.8   1699 9   HSM801509   AL133659     120   17.8   1782 9   BC025776   AB070110   Macaca     120   17.8   2003   17 AF130092   AF130092   AF130092     120   17.8   2004 9   BC014433   AR059958   BC014433   Homo Sa     120   17.8   2105 9   HSM801370   AL832397   Homo Sa     120   17.8   2105 9   HSM801370   AL832397   Homo Sa     120   17.8   2194   BC027927   BC027927   Homo Sa     120   17.8   2499 9   HSM801350   AL33308   Homo Sa     120   17.8   2633 9   HSM801350   AL83308   Homo Sa     120   17.8   2633 9   HSM801350   AL83308   Homo Sa     120   17.8   2639 9   HSM801373   AL83266   Homo Sa     120   17.8   6171 6   AX351820   AX35182   Sequence     120   17.8   6577 6   AX35187   AX35187   Sequence     120   17.8   6577 6   AX344861   AX344861   Sequence     120   17.8   8699 6   AX344861   AX344861   Sequence     120   17.8   8999 6   AX344861   AX348813   Sequence     120   17.8   8999 6   AX344861   AX348813   Sequence     120   17.8   8999 6   AX344861   AX34591   Sequence     120   17.8   8999 6   AX344861   AX345813   Sequence     120   17.8   8999 6   AX34861   AX345813   Sequence     120   17.8   8999 6   AX34861   AX348813   Sequence     120   17.8   8999 6   AX34861   AX348813   Sequence     120   17.8   8999 6   AX34861   AX3488913   Sequence     120   17.8   8999 6   AX34861   AX3488913   Sequence     120   17.8   B996 6   AX34861   AX3458913   Sequence     120   17.8   B996 6   AX34861   AX3458913   Sequence     120   17.8   B996 6   AX34861   AX3488893   Sequence     120   17.8   B996 6   AX34861   AX34888913   Sequence     120   17.8   B996 6   AX34861   AX34888913   Sequence     120   17.8   B996 6   AX34861   AX34888913   Sequence     120   17.8   B996 6   AX3488913   AX34888913   Sequence     120	16	120	_		0	BC016152	2 6
120   17.8   1699   9   HSM801509   AL133540   HGMC SEC     120   17.8   1728   9   AB005420   AB0056420   AB00504433   HGMC SEC   AB0056420   AB005044433   HGMC SEC   AB0056420   AB005044433   HGMC SEC   AB0050420   AB0050440   AB0	17	120	_ `		0	BC028121	2 6
120   17.8   17.8   9 AB070110   BC025776   Homo States   120   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8   17.8	18	120			σ,	HSM801509	ě
120   17.8   2003   17.8   2003   2 AB056420   AEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE	5 C	120	· ·		σ (	AB070110	CBC
120   17.8   2003   17 API30092   AR050420 Homoses   2003   17.8   2004   9 BC014433 Homoses   2007   17.8   2008   6 AR059958   BC014433 Homoses   2008   6 AR059958   BC014433 Homoses   2008   6 AR0599370   AR0599370   AR0599370   Sequency   2008   2008   6 AR099370   AR0599370   Sequency   2009   17.8   2194   10 BC031202   BC031202 Mus m	2.5	120	٠.		ס ע	BC025/76	OEC
120   17.8   2074   9   BCO14433   BCO131202   ALB32397   Homo sagistic   17.8   2194   10   BCO31202   BCO3	22	120	'		, [	AB036420 AF130092	Sca
120   17.8   2082 6   AR059958   AR059937   AR099370   AR099070   AR099370	23	120			io	AL 130032 BC014433	
120   17.8   2105 9   HSR803705   ALB32397   Homo sage     120   17.8   2196   G   AX099370   AX099370   AX099370     120   17.8   2194   D   BC027927   Homo sage     120   17.8   2447   9   BC027927   Homo sage     120   17.8   2499   9   HSR801350   ALB333016   Homo sage     120   17.8   2691   9   BC03556   BC027927   Homo sage     120   17.8   2691   9   BC035271   BC0330556   Homo sage     120   17.8   4518   9   HSR80373   ALB333016   Homo sage     120   17.8   4518   9   HSR803128   ALB331016   Homo sage     120   17.8   6577   6   AX345659   AX345659   Sequence     120   17.8   6577   6   AX346258   AX346558   Sequence     120   17.8   6577   6   AX346258   AX344560   AX344560     120   17.8   6794   6   AX348651   AX344560   AX344560     120   17.8   6794   6   AX348651   AX344560   AX344560     120   17.8   6794   6   AX348651   AX344560   AX348651   Sequence     120   17.8   6899   6   AX34539   AX348651   Sequence     120   17.8   8899   6   AX34539   AX345539   AX345539     120   17.8   8899   6   AX34539   AX345539   AX345539     120   17.8   8899   6   AX34539   AX345539   AX345539     120   17.8   8899   6   AX345539   AX345539   AX345539   AX345539     120   17.8   8899   6   AX345539   AX345539   AX345539   AX345539     120   17.8   8899   6   AX345539	24	120			9	AR059958	
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120 17.8 4194 10 BC031202 Mus mus 120 17.8 4199 9 HSM801350	976	120	•		ω;	AX099370	dae
120   17.8   249   9   15.02.7927   ALI333016   Homo Sagi 120   17.8   249   9   15.02.7927   ALI333016   Homo Sagi 120   17.8   2991   9   15.02.0556   Homo Sagi 120   17.8   2991   9   15.02.0556   Homo Sagi 120   17.8   3005   10   10   10.02271   Homo Sagi 120   17.8   4930   9   HSM803971   ALB33066   Homo Sagi 120   17.8   4930   9   HSM803973   ALB33066   Homo Sagi 120   17.8   5152   9   HSM803128   ALB31816   Homo Sagi 120   17.8   6577   6   AX251920   AX344260   AX34	28	120	•		010	BC031202	(ns
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120   17.8   2991   9   BC030556   BC030256   Homo sage     120   17.8   4930   9   BC032271   BC032271   Mus mus     120   17.8   4930   9   HSM803973   AL832066   Homo sage     120   17.8   4930   9   HSM803128   AL832066   Homo sage     120   17.8   6171   6   AX34590   AX345690   AX345690   Sequence     120   17.8   6577   6   AX34893   AX34658   Sequence     120   17.8   6577   6   AX34893   AX34893   Sequence     120   17.8   6794   6   AX34893   AX348651   Sequence     120   17.8   6794   6   AX348651   AX348651   Sequence     120   17.8   6794   6   AX348651   AX348651   Sequence     120   17.8   6899   6   AX348651   AX348651   Sequence     120   17.8   8899   6   AX348651   AX348651   Sequence     120   17.8   8899   6   AX348651   AX348651   Sequence     120   17.8   8899   6   AX345813   AX345813	30	120			י ס	HSM804701	
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120   17.8   4918   9   HSN8002971   AL713745   Homo sag   120   17.8   4930   9   HSN8003973   AL831066   Homo sag   120   17.8   5152   9   HSN8003128   AL831066   Homo sag   120   17.8   5152   9   HSN8003128   AL831065   Sequence   120   17.8   6577   6   AX346258   AX346259   AX346259   AX346259   AX346259   AX348093   AX346259   AX346259   AX346259   AX346259   AX346259   AX346250   AX34625   AX346250   AX34620   AX346250   AX346250   AX346250   AX346250   AX346250   AX34620   AX346250   AX346250   AX346250   AX346250   AX346250   AX34620   AX	M (	120	•		10	BC032271	en.
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120   17.8   6577   6   AX251920   AX251920   Sequence   120   17.8   6577   6   AX346258   AX346528   AX346528   AX346528   AX346993   AX346993   Sequence   120   17.8   6794   6   AX344260   AX34450   AX344560   Sequence   120   17.8   6794   6   AX3448651   AX344651   AX344651   AX34651   Sequence   120   17.8   8899   6   AX348651   AX348651   AX348651   Sequence   120   17.8   8899   6   AX348651   AX348651   AX348651   Sequence   120   17.8   8899   6   AX345813   AX348651   Sequence   120   17.8   8899   6   AX345813   AX34861   Sequence   120   17.8   88946   6   AX345813   AX345813   Sequence   120   17.8   Sequence   120   AX345813   Sequence   AX345813   Sequence   120   AX345813   Sequence   AX345813	m	120			v د	AX345690	das omo
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ALIGNMENTS  HSW802993  AL713659  AL713659  AL713659.1 GI:19584343  human.	4	120			9	4X345813 ·	daeuc
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HSM802993 3454 bp mRNA linear PRI 20-MAR-2 NN Homo sapiens mRNA; cDNA DKFZp667D1012 (from clone DKFZp667D1012) A AL713659 AL713659.1 GI:19584343 human.	·			٠			
M Homo Sapiens mRNA; cDNA DKFZp667D1012 (from clone DKFZp667D1012) AZ713659.1 GI:19584343 human.	SM802993 OCUS		,2993			3454 bp mRNA	PRI 20-MAR-2
human.	CCESSION FRSION	z	sap1 1659 1659	S mRNA	0	DKFZp667D1012 (from	DKFZp667D1012)
	EYWORDS		1.6500	1:13	•		
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Genome CA 94305

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Mus musculus, RIKEN CDNA 2810429K11 gene, clone MGC:31645
IMAGE:4527027, mRNA, complete cds.
                                                                                                                                                                                                                                                                                      information can be found
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Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg, R.
Direct Submission
Submitted (02-JUL-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                              WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Pravyed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 943
Web site:
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution information can be fou through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: RAL Plate: 16 Row: p Column: 18 This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not
nstitute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="rwAGE:4052341"
/tissue_type="Ridney, hypernephroma"
/clone_lib="NIH_MGC_58"
/lab_host="DH108"
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17.9%; Score 121; DB 9; I
Llarity 100.0%; Pred. No. 7.3e-55;
Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
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82 c 107 g 123
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Mammalia, Eutheria, Rodentia;
1 (bases 1 to 2776)
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Location/Qualifiers
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BC034120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="HTGERPYSCLKCEKTFGRRHHLIRHQKTHLHDKTSRCSECGKNFROSHLASHQRVHAEGKSCKGQEVGESPGTRKRPRAPPVPKCHVCTECGKSFGRRHHLLVHWLTHTGEKPFQCPRCEKSFGRKHHLDRHLLTHQGQSPRNSWDRGTSVF"
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      Martinsried, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by BMFZ (Blomedical Research Center at the Charite,
Berlin/Germany) within the cDNA sequencing consortium of the German
Genome Project.
                                                                                                                            This clone (DKFZp667D1012) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://mips.gsf.de/proj/cDNA/.
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Catarrhini; Hominidae; Homo.
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Submitted (25-MAY-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
                                                                                                                                                                                                                                                                                                                                  /tissue_type="lymph node" /clone_lib="667 (synonym: hlno2). Vector pSportl; host DH10B; sites NotI + SalI" /dev_stage="adult" | 1.3454
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/db_xref="taxon:9606"
/map="295.8 cR from top of Chr12 linkage group"
/clone="DKFZp667D1012"
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0. 2.2e-55; Indels
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/codon_start=3
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/protein_id="CAD28468.1"
/db_xref="G1:19584344"
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100.0%; Pred. No. 2.26
-100.0%; Mismatches
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/gene="DKFZp667D1012"
3306
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Mammalia; Eutheria;
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Best Local Similarity 100.0
Matches 122; Conservative
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Best Local Similarity 100.
Matches 121; Conservative
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HSM803701
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/product="RIKEN CDNA 2810429K11 gene"
/product="121707639"
/db_xref="121707639"
/db_xref="1217077"
/db_
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site:
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                         can be found
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:10090"
/clone="MGC:31645 IMAGE:4527027"
/tissue_type="Eyg, retina, mouse strain C57Bl\6"
/clone_ltb=host="DH10B"
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Pred. No. 7.8e-55;
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100.0%; Pred. No. ...
0; Mismatches
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Best Local Similarity 100.
Matches 121; Conservative
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Submitted (09-JUL-2002) 1, D-85764 Neuherberg, GERWANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (0KF2): Email s.wiemann@dkfz-heidelberg.de;
Sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
consortium of the German Genome Project.
This clone (DKF266860316) is available at the RZDD in Berlin.
Please contact the RZDD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERWANY: Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at http://mips.gsf.de/proj/cDNA/.
                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="krspe@860010"
/clone_lib="686 (synonym: hlcc3). Vector pSportl_Sf1; host /dev_stes Sf11A + Sf11B"
2686. 2691
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ALB32393.1 GI:21732956
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1 (bases 1 to 2830)
Wambutt,R., Heubner,D., Mewes,H.W., Well,B. and Wlemann,S.
Direct Submission
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Koehrer, K., Beyer, A., Mewes, H.W., Well, B. and Wiemann, S.
Direct Submission
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BC034163.1 GI:21706753
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TITLE
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 /clone="DKFZp667K1712"
/tissue_type="lymph node"
/clone_lib="667 (synonym: hlno2). Vector pSportl; host
DH10B; sites NotI + SalI"
321. 3236
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Diagnosis of diseases associated with angiogenesis
Diagnosis of diseases associated with angiogenesis
Patent: WO 0246454-A 80 13-JUN-2002;
Epigenomics AG (DE)
Location/Qualifiers
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Pred. No. 7.9e-55;
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/db_xref="taxon:32630"
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artificial sequences
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Matches 121; Conservative
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AKO26865 1034 bp mRNA linear PRI 29-SEP-2000 Homo sapiens CDNA: FLJ2312 fis, clone ADSU01518, highly similar to AF182844 Homo sapiens VPS28 protein mRNA.
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Contact: MGC help desk

Email: cgapbs-rémail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

BAS Sequencing by: Sequencing Group at the Stanford Human Genome

Center, Stanford Viscousity School of Medicine, Stanford, CA 94305.

Web site: http://www-shgc.stanford.edu

Contact: (Dickson, Mark) mcd@paxil.stanford.edu

Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,

R. M.
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/db_xref="LocusID:14127"
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                                            Mus musculus Eukaroos; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Criurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 800)
Strausberg, R.
Strausberg, R.
Submission
Submitted (02-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="Mammary tumor metastatized to lung. rumor arose spontaneously from a senescent normal mammary (closal) outgrowth infected with the virus MMTV." /close_lib="MYCL_CGAP_Lu29" /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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llarity 100.0%; Pred. No. 2.6e-54;
Conservative 0; Mismatches 0;
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/db_xref="taxon:10090"
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/db_xref="G1:21706754"
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Best Local Similarity
Matches 120; Conserv
house mouse.
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/product-"Similar to myoglobin"
/product-"de-"AAH14547.1"
/db_xref-"de-"AAH14547.1"
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DKFKHLKSEDEWKASEDLKKKHGATVLTALGGILKKKGHHEAEIKPLAGSHARKHKIPV
KYLERISECTIQVLGSKHPGDFGAANGAANKALELFRKDMASNYKELGFQG"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
Greene, Mark Ketteman and Anuradha Madan
                                                                                                                                                                                                                                                                                                                                                       Clone distribution: MGC clone distribution information can be foun through the I.M.A.G.E. Consortium/LIML at: http://image.llnl.gov Serles: IRAL Plate: 19 Nov g Column: 18 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4885476.
          Direct Submission
Submitted (24-SEP-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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                                                                                                            NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-rémail.nih.gov
Tissue Procurement: CLONTECH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="MGC:13548 INAGE:4244838"
/tissue_type="Skeletal Muscle"
/clone_lib="NHH_MGC_81"
/lab_host="DH108"
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100.0%; Pred. No. 2.6e-54;
tive 0; Mismatches 0;
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67, Last updated, Version 2)
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Matches 120; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                               Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genier; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnaidims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)

NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; CDNA full insert construction; Research Association for Biotechnology; CDNA library Construction, 5'- & 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens, Similar to myoglobin, clone MGC:13548 IMAGE:4244838, BC014547
                                                                                                                                                         1 (sites)
Kawakami,T., Noguchi,S., Itoh,T., Shigeta,K., Senba,T.,
Matsumura,K., Nakajima,Y., Mizuno,T., Morinaga,M., Tanigami,A.,
Fujiwara,T., Ono,T., Yamada,K., Fujii,Y., Ozaki,K., Hirao,M.,
Ohmori,Y., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T.,
Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
NEDO human cDNA sequencing project
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1191)
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Shibahara,T., Tanaka,T. and Nakamura,Y.
Direct Submission
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                                      oligo capping; fis (full insert sequence).
Homo sapiens adipose tissue cDNA to mRNA, clone_lib:ad
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100.0%; Pred. No. 2.6e-54;
.1ve 0; Mismatches 0; Indels
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/note="highly similar to AF182844
protein mRNA"
1 289 c 264 g 166 t
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/tissue_type="adipose tissue"
/clone_lib="ad"
/note="Cloning vector pME18SFL3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
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                                                                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Matches 120; Conservative
                                                                          clone: AbSU01518.
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BC016332 1388 bp mRNA linear PRI 05-NOV-2001 Homo sapiens, ubiquitin-conjugating enzyme E2 variant 2, clone MGC:23763 IMAGE:4109228, mRNA, complete cds.
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GARGSTAAQMSQALCLYKDGDIHRGFOSLLSEVNRTGTQYLLRTANRLFGEKTCDFLP
DFREYCOKFYQAELEELSFAEDTECRKHINDWYAEKTEGKISEVLDAGTVDPLTKLY
LVNAIYFKGKWNEQFDRYTRGMLFKTNEEKKTVQMMFKEAKFKMGYADEVHFGVLEL
PYVBEELSWYILLDDNYTDLAYKE"

250 c 279 g 310 t
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1388)
                                                                                                                                                                                                                                                    through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 29 Row: m Column: 11
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 4505790.
Location/Qualifiers
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Direct Submission
Submitted (29-OCT-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                     X., Hulyk, S.W., Hale, S.M., S., Martin, R.G., Muzny, D.M.
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inhibitor, clade B (ovalbumin), member 8"
/protein_id="AAH34528.1"
/db_xref="G1:21961225"
                                                                                                                                                                                                                               Clone distribution: MGC clone distribution information can
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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/clone="Mosc:14899 INAGE:4780455"
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/clone_lib="NCI_CGAP_Skn3"
/lab_host="DH10B"
                               Web site: http://www.hgsc.bcm.tmc.edu/cdna/
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ilarity 100.0%; Pred. No. 2.7e-54;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pCMV-SPORT6.ccdb"
                                                               Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu,
Ycon, V.S., Kowis, C.R., Lawrence,
Richards, S., Gibbs, R.A.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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       Center code:
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1319)
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Submitted (24-JUL-2002) National Institutes of Health, Mammalian
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Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Medicine,
                                                                                                                                                                                                                                                                                                                                                                            Zhang C., Yu Y., Zhang S., Ouyang S., Luo L., Wei H., Zhou G., Zhou W. Bi J., Zhang Y., Liu M., He F.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (14-DEC-1998) to the EMBL/GenBank/DDBJ databases.
Department of Experimental Hematology, Institute of Radiation
Beijing Taiping Road 27, Beijing 100850, P. R. China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1298;
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Pred. No. 2.7e-54;
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100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"/clone="FLB4701"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9606"
/note="HQ1219"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="liver"
/dev_stage="fetus"
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nes 120; Conservative
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BC034528
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Best Loca Matches

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RESULT 11 BC034528

ORGANISM ACCESSION VERSION KEYWORDS SOURCE

TITLE JOURNAL

REMARK COMMENT

REFERENCE AUTHORS

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Gaps

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Length 1319; Indels

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BC032462
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JOURNAL
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                                                                                                              Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plates 32 Row: b Column: 4 This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="ubiquitin-conjugating enzyme E2 variant 2"
/protein_id="AAH16332.1"
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IPVLAKWQNSYSIKVVLQELRRLMMSKENMKLPQPPEGQTYNN"
179 c 271 g 346 t
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Contact: MGC help desk
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BC006018 1462 bp mRNA linear ROD 07-AUG-2002 Mus musculus, MyoD family inhibitor, clone MGC:5939 IMAGE:3488088,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1462)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (02-APR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                       /db_xref="tocusid:7336"
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/db_xref="tocusid:7336"
/tissue_type="Bone marrow, acute myelogenous leukemia"
/clone_lib="NHH_MGC_55"
                                                               Mark Ketteman, Anuradha
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                                                                                    and Michelle Whiting
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Pred. No. 2.7e-54;
DNA Sequencing by: Institute for Systems Biology http://www.systemsbiology.org contact amadan@systemsbiology.org Anup Madan, Jessica Fahey, Erin Helton, Mark Keti Madan, Stephanle Rodrigues, Amy Sanchez and Michi
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                                                                                                                                                                                                                                                    1. .1388
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pDNR-LIB
                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                              /lab_host-"DH10B
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
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BC006018
BC006018.1 GI:13543726
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Matches 120; Conservative
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Direct Submission
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TITLE
JOURNAL
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BC006018
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/organism="Mus musculus"
/db_xref="taxon:10090"
/db_xref="taxon:10090"
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/clone="MGC:5939 IMAGE:3488088"
/tissue_type="Mammary tumor: WAP-TGF alpha model. 7 months old, gross tissue."
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EDCCVHGILSGLFCEFLTLGNILLDATGGSCSSEDSCLCCCCGGGECADCDLPCDL
DCGIVDACCESADCLEICMECGGLCFSS"
423 c 407 g 249 t
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                                                                                                                      Clone distribution: MGC clone distribution information can be foun through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRMX Plate: 7 Row: o Column: 10 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6754665. Location/Qualifiers
Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostoml;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (06-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gapa
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MGC:40428 IMAGE:5197243, mRNA, complete cds.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="MyoD family inhibitor"
/protein_id="AAH06018.1"
/db_xref="GI:13543727"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17.8%; Score 120; DB 10;
100.0%; Pred. No. 2.7e-54;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pCMV-SPORT6"
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BC032462.1 GI:21595557
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Best Local Similarity 100.0
Matches 120; Conservative
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Beguin, P
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                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 64 Row: h Column: 20 This clone was selected for full length sequencing because it passed the following selection criteria: GenomeScan gene prediction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="Myraavaatkawisggvircwepwggrgrgigksrrprggpga
Glgkaokrsregrerpplgaaglgivsrpggarghprgkkaplaarpytrharpsggr
Plvixiecsgdrgtvirfotvptrfpgkappagwgvvveaglsdaegevasrisypfn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Neb site: http://www.nisc.nih.gov/
Akhter.N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,K., W., Bouffard,G., Breen,K., Brikkley,C., Brooks,S.,
Blakesley,K.,W., Bouffard,G.G., Breen,K., Brikkley,C., Brooks,S.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brikkley,C.,
Brooks,S.,
Hansen,N.L., Granite,S., Guan,X., Gupta,J., Hadpighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Beguin,P., Wang,X., Firsov,D., Puoti,A., Claeys,D.,
Horisberger,J.D. and Geering,K.
The gamma subunit is a specific component of the Na,K-AIPase and
modulates its transport function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gamma subunit of sodium potassium ATPase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="Brain, adult, 6 pooled whole brains"
/clone_lib="NIH_MGC_l14"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="hypothetical gene supported by BC017964"
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  Sequencing by: National Institutes of Health Intramural
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X.laevis mRNA for Na,K-AFPase gamma subunit.
Y11587
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'Organism="Homo sapiens"

/db_xref="LocusID:144714"

/db_xref="taxon:9606"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17.8%; Score 120; DB 9; I 100.0%; Pred. No. 2.7e-54; tive 0; Mismatches 0;
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ATPase; gamma subunit;
NA+, K+-ATPase.
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Xenopus laevis
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VERSION
KEYWORDS
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XLNAKATP
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/translation="WADAQDDMSQMQDKFTYDYETIRKGGLIFAAIAFVVGMLIIFSG
RFRCGRKKQLRALNDDM"
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                                                                                      Direct Submission
Submitted (26-FEB-1997) P. Beguin, University of Lausanne,
Institute of Pharmacology and Toxicology, Rue du Bugnon 27, 1005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1500;
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                                                                                                                                                                                                                                                                                         /product="gamma subunit of Na,K-ATPase"
/protein_id="CAA72326.1"
/db_xref="G1:2052284"
                                                                                                                                                                                                                                                                                                                                                                                                                                          tch 17.8%; Score 120; DB 5; I al Similarity 100.0%; Pred. No. 2.7e-54; 120; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                      /db_xref="SWISS-PROT:013001"
                                                                                                                                                                                                                                                                                                                                                                                            432 t
                                                                                                                                                                                   /organism="Xenopus laevis"
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EMBO J. 16 (14), 4250-4260 (1997) 97392454
                                                                                                                                                                                                                                         /tissue_type="kidney"
63. .248
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Job time : 2000.2 secs
                                                                                                                                                      Location/Qualifiers
1. .1500
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                                                   (bases 1 to 1500)
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Best Local Similarity
Matches 120; Conserv
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Title: Perfect score:

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Run on:

Scoring table:

Word size Searched:

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Human secreted pro
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Human immune syste
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Human immune syste
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Human ovarian and
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Mouse neuronal
                              DNA encoding
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                                                                                                                          AAV41257
AAF98380
ABL32788
                                                                                                                                                                   ABL70561
ABL33356
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AAK78761
AAK79574
AAK81312
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ABL32837
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AAS45399
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2000US-189862P.
2000US-207454P.
2000US-211314P.
2000US-219007P.
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                          804
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1097
1194
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2108
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6577
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15832
15832
40324
 WO200160860-A2
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25-MAY-2000; 2
09-JUN-2000; 2
18-JUL-2000; 2
13-DEC-2000; 2
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Human secreted pro
Human cDNA encodin
Human polynuclecti
Human ngiogenesis
Human prostate exp
Human prostate exp
Human prostate exp
                                                                            June 16, 2003, 03:58:29; Search time 222.269 Seconds (without alignments) 6849.143 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                     1. SIDSZ/gcgdata/geneseq/geneseqn-embl/NA1980. DAT:*
2. SIDSZ/gcgdata/geneseq/geneseqn-embl/NA1981. DAT:*
3. SIDSZ/gcgdata/geneseq-embl/NA1981. DAT:*
4. SIDSZ/gcgdata/geneseq-embl/NA1982. DAT:*
5. SIDSZ/gcgdata/geneseq-embl/NA1982. DAT:*
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                                                                                                                                     Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:
    GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                       rotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                     2185239 seqs, 1125999159 residues
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                                                       - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                               Post-processing: Listing first 45 summaries
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AAC60033
AAS31262
ABQ66586
ABQ67050
ABV5006
ABV58008
ABV58809
                                                                                                                                                                                             OLIGO_NUC
Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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Schlegel R, Endege WO, Monahan JE;

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Komatsoulis G;

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Rosen CA, Ruben SM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                     selecting a composition for inhibiting prostate cancer in a patient; assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastasized in a patient; assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; secreted protein; neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular; vulnerary; gastrointestinal; nephrotropic; antibactive; gynaecological; antibacterial; neural disorder; cancer; immune disease; reproductive disorder; proliferative disorder; gastrointestinal disease; wound healing; infectious disease;
                               Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                                                                                                         (d) assessing the efficacy of a therapy for inhibiting prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                              (I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
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                                                                                                                                                                                                                                                                                                                                                                                        Length 381;
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                                                                                                                                                                                                                                                                                                                                                          Sequence 381 BP; 196 A; 70 C; 49 G; 66 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                        Score 121; DB 23;
Pred. No. 3.2e-28;
                                                                                                                                                                                                                                                                                                                                                                                17.9%; Scor.
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human secreted protein gene 9 SEQ ID NO:19.
                                                                                             Claim 1; Page 11255; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAC60033 standard; cDNA; 1119 BP.
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99US-0168664.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 121; Conservative
                                                                                                                                                                       (a) assessing whether(b) monitoring the pr(c) assessing the effcancer in a patient;
       WPI; 2001-662795/76.
                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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03-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                            Best Local
                                                                                                                                                                                                                                                                                                                     patient
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The polynucleotide sequences given in AAC60025-C60071 encode the human secreted proteins represented in AAB34854-B34900. Sequences AAB34901-B34976 are fragments of proteins encoded by the genes, and also proteins with which they share sequence homology. The proteins have cartivities based on the tissues in which their encoding genes are activities based on the tissues in which their encoding genes are activities based on the tissues in which their encoding genes are crivities proteins activity; general gastrointestinal activity; nephrotropic; vulnerary; general gastrointestinal activity; nephrotropic; antiinfective; gynaecological; and antibacterial. The human secreted proteins, polynucleotides, antagonists and antagonists of the invention can be useful in treating, preventing and/or diagnosing various diseases, disorders and conditions such as neural, immune, miscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and confidentive disorders and cancer. They may also be used in the treatment of wounds, and infectious diseases. The polypeptides may be seed as a food additive or preservative to increase storage capabilities. Sequences AAC60016-C60024 and AAB34853 are used in the course of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; secreted extracellular matrix protein; ss; immunomodulatory; Anti-HIV; antianemic; antirheumatic; antisclerotic; cardiant; vascular; cerebroprotective; thrombolytic; antimicrobial, ophthalmic; cytostatic; antialzhelmers; immune/autoimmune disease; HIV infection; anaemia; human immunodeficiency virus; rheumatoid arthritis; multiple sclerosis; cancers; hyperproliferative disorder; breast neoplasm; melanoma; Sezary syndrome; Gaucher's disease; neurological diseases; Alzheimer's disease; Parkinson's disease; cardiovascular disorder; cardiac arrest; tachycardia; angina; infection; corneal infections; wound healing; immunogen; gene therapy; antisense; food additive.
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                                                                                      Human secreted proteins and gene sequences encoding them, useful for detection, prevention, and treatment of various disorders such as cancer and immune system disorders -
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                                                                                                                                                                                                                                                                   Claim 1; Page 355; 442pp; English.
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2000-594574/56
                                     P-PSDB; AAB34862
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Ruben SM
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20000S-0241809
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20000S-0244617
20000S-0246474
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20000S-0246477
20000S-0246477
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20000S-0246524
20000S-0246527
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20000S-0246526
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    20000S-0179065
2000US-0184664
2000US-0184664
2000US-0186350
2000US-0199076
2000US-0199076
2000US-0198123
2000US-020515
2000US-020515
2000US-0216886
2000US-0216886
2000US-0216886
2000US-0216880
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2000US-0216880
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20000S-0229345.
20000S-0229509.
20000S-0229509.
20000S-0230437.
                        17-JAN-2001; 2001WO-US01348
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2000US-0235836
WO200155368-A1.
            02-AUG-2001
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17-JAN-2001; 2001US-0764870
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            11-APR-2002
ovel human secreted extracellular matrix proteins (SPs). The polynucleotides and proteins are used to prevent, treat a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. For example, disorders associated with decreased expression of SPs. The SP polynucleotide or a vector expressing them may be administered to down regulate expression of SPs by binding with the cells own genes and preventing their expression. The polynucleotides may also be used as DNA probes in diagnostic assays. The SPs may also be used as DNA probes in diagnostic assays. The SPs may also be used to down regulate expression and activity of antagonists may also be used to down regulate expression and activity of special and as diagnostic agents for detecting the presence of SPs in samples. The disorders include for example: Immune/autoimmune disoases (e.g. HIV the disorders include for example: Immune/autoimmune disoases (e.g. MIV the disorders include for example: Immune/autoimmune disoases (e.g. MIV the disorders disease), neurological diseases (e.g. Alzheimer's disease, cand multiple sclerosis), cancers and hyperproliferative disorders (e.g. cardiac arrest, tachycardia and angina), infections caused by bacteria, viruses and fungi and ocular disorders (e.g. corneal infections). Other uses include wound healing, maintenance of organs before transplantation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; crebroprotective; antiinflammatory; antiallergic; antidiabetic; antibucer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder;
                                                                                proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers
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                                                                      Nucleic acid molecules encoding human secreted extracellular matrix
                                                                                                                                                                        invention relates to isolated nucleic acid molecules encoding
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100.0%; Pred. No. 1.7e-28;
tive 0; Mismatches 0;
                                                                                                                                        Claim 1; SEQ ID No 76; 577pp; English.
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Best Local Similarity 100.
Matches 121; Conservative
                       WPI; 2001-465572/50.
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                                     P-PSDB; AAU19691
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The invention relates to novel genes (ABO66521-ABO66785) and proteins (ABP47846-ABP48110) useful for preventing, treating or ameliorating
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2000US-217496P.
2000US-218290P.
2000US-220963P.
2000US-220964P.
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P-PSDB; ABP47911.
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(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
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02-OCT-2000;
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The invention relates to a nucleic acid (I) comprising a segment of 18 bases of chemically pretreated DNA of angiogenesis-associated genes (II) having sequences (ABG66971-ABG6719) or their complements. (I). also related oligomers, are used to evaluate the methylation status and/or single-nucleotide polymorphisms, in angiogenesis-related genes, for diagnosis and treatment of eye diseases, proliferative retinopathy, necowascular glaucoma, solid tumours, inflammation, rheumatoid arthritis, diabetic retinopathy, macular degeneration caused by neovascularisation, ground's disease.

Crohn's disease.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formet directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; prostate cancer;
pharmacogenomic marker;
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09-JUN-2000;
18-JUL-2000;
13-DEC-2000;
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medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, crohn's clease, multiple sclerosis, rheumatoid arthritis and ulcerative colities; (c) cardiovascular disorders such as myocardial ischaemias;
                                                                                                                                                                           (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; anglogenesis; methylation; eye disease; glaucoma; tumour;
inflammation; rheumatoid arthritis; diabetic retinopathy; antiulcerds;
macular degeneration; inflammatory bowel disease; Crohn's disease;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
                                                                                                                                                                                                                               Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata uspto.gov/sequence.html?DocID=9999909764870.
                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                               Length 2645;
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                                                                                                                                                                                                                                                                                                     Sequence 2645 BP; 827 A; 506 C; 513 G; 799 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                          17.9%; Score 121; DB 24;
100.0%; Pred. No. 1.7e-28;
11ve 0; Mismatches 0;
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ID ABQ67050 standard; DNA; 6486 BP.
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Matches 121; Conservative
                                                                                                                                                                                                                  and parasitic infections.
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                                                                                                                                                                                                                                                                                                              cytostatic; carcinogen; pharmacodyanamic marker; gene; ss.
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                                                                              Gaps
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                                         Length 6486;
                     Sequence 6486 BP; 1713 A; 176 C; 1443 G; 3154 T; 0 other;
                                                               Indels
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                                        17.9%; Score 121; DB 24;
100.0%; Pred. No. 1.3e-28;
1ve 0; Mismatches 0;
at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                Human prostate expression marker cDNA 50197.
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2000US-189862P.
2000US-207454P.
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2000US-219007P.
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                                     Query Match
Best Local Similarity 100.C
Matches 121; Conservative
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nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of
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09-JUN-2000;
18-JUL-2000;
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16-MAR-2000;
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           The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                      9/9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid molecule (I) comprising
                                                                                                     selecting a composition for inhibiting prostate cancer in a patient; assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastassized in a patient; assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                              Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                              (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
                                                                                                                                                                                                                                                                                      Gaps

    is also useful as a pharmacodyanamic or pharmacogenomic marker.

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                                                                                                                                                                                               Length 439;
                                                                                                                                                                                                                   Indels
                                                                                                                                                                             Sequence 439 BP; 179 A; 117 C; 69 G; 69 T; 5 other;
                                                                                                                                                                                     17.8%; Score 120; DB 23;
100.0%; Pred. No. 6.1e-28;
0;
                                                                                                                                                                                                                                                                                                                                                                                                           Human prostate expression marker cDNA 59273.
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                                                                                                                                                                                                        al Similarity 100.0%; Pred. No. 6.1 120; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                         gene; ss
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2000US-207454P.
2000US-211314P.
2000US-219007P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         pharmacogenomic marker;
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                                                                             cancer in a patient;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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                                                                                                                                                  patient;
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                                                                                                          (e)
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(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate cell carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a

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                                                                                                                                               (d) assessing the efficacy of a therapy for inhibiting prostate cancer
in a patient;
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specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 452 BP; 199 A; 91 C; 72 G; 89 T; 1 other;
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Best Local Similarity 100.0%; Pred. No. 6e-28;
Matches 120; Conservative 0; Mismatches (
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2000US-189862P.
2000US-207454P.
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                                                                                                                                      cancer in a patient;
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18-JUL-2000;
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Matches 120;
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                                                                                                                                         Query Match
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                                                in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate cell carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     comprising
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                       (d) assessing the efficacy of a therapy for inhibiting prostate cancer
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                                                                                                              (I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
assessing whether a patient is afflicted with prostate cancer; monitoring the progression of prostate cancer in a patient, assessing the efficacy of a test compound to inhibit prostate
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(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
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                                                                                                                                                           Length 484;
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                                                                                                                                   Sequence 484 BP; 230 A; 97 C; 82 G; 74 T; 1 other;
                                                                                                                                                        17.8%; Score 120; DB 23;
100.0%; Pred. No. 5.9e-28;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                            Human prostate expression marker cDNA 55880,
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                                                                                                                                                                                                                                                                                                              ABV55889 standard; cDNA; 516
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2000US-207454P.
2000US-211314P.
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                                                                                                                                                                 Local Similarity 100.
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 (a) assessing whether (b) monitoring the pr (c) assessing the eff cancer in a patient;
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25-MAY-2000;
09-JUN-2000;
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13-DEC-2000;
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Matches
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(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate cell carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a patient;
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pharmacogenomic marker; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                           17.8%; Score 120; DB 23; Length 516; 100.0%; Pred. No. 5.8e-28; ative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                               Sequence 516 BP; 239 A; 93 C; 91 G; 93 T; 0 other;
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2000US-189862P.
2000US-207454P.
2000US-211314P.
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WO200155326-A2
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                        selecting a composition for inhibiting prostate cancer in a patient; assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastasized in a patient; assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
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(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
assessing the efficacy of a therapy for inhibiting prostate cancer
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                                                                                                   (I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
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                                                                                                                                                        Length 544;
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                                                                                                                              Sequence 544 BP; 220 A; 141 C; 97 G; 84 T; 2 other;
                                                                                                                                                           Score 120; DB 23;
Pred. No. 5.7e-28;
                                                                                                                                                17.8%; Scor.
100.0%; Pred. No. 5...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human prostate expression marker cDNA 58681.
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                                                                                                                                                                                                                                                                                                                                                                           ABV58690 standard; cDNA; 579 BP.
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2000US-207454P.
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2000US-219007P.
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                                                                                                                                                                       Similarity
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                   in a patient
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Best Local 9
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                                                                                          patient
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Matches
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ABV58690
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The invention relates to novel isolated nucleic acid molecules (I) encoding human secreted proteins (II). (I) and (II) are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. (I) and (II) may be used the prevention, treatment and diagnosis of diseases associated with inappropriate expression of secreted proteins. (I) and complementary sequences may also be used as DNA probes in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect and quantitate the presence of similar nucleic acid sequences in samples, and so which patients may be in need of restorative therapy. (II) may also be used as antigens in the production of antibodies and in assays to identify modulators
                                                                                                                                                                                                                                                                                                                                                                                  Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                       616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           selecting a composition for inhibiting prostate cancer in a patient; assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastasized in a patient; assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acids and polypeptides, useful for diagnosing, preventing or treating medical conditions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunomodulatory; human immunodeficiency virus; HIV; anaemia; angina; rheumatoid arthritis; antiarteriosclerotic; cardiant; vascular; cerebroprotective; thrombolytic; antimioroblal; ophthalmological; cytostatic; Alzheimer's disease; Parkinson's disease; human; cancer; multiple sclerosis; cancer; hyperproliferative disorder; infection; Gaucher's disease; neurological disease; cerebrovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                 (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                    Length 579;
                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                               Sequence 579 BP; 269 A; 106 C; 82 G; 121 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding human secreted protein, Seq ID No 107.
                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                    Score 120; DB 23;
Pred. No. 5.6e-28;
                                                                                                                                                                                                                                                                                                                    Ouery Match
17.8%; Score 120; DB
Best Local Similarity 100.0%; Pred. No. 5.6
Matches 120; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAS33148 standard; cDNA; 804 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     thrombosis; wound healing; ss.
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P-PSDB; AAU20439.
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us-10-090-035-1.rng

10-MAY-2001

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consists and antagonists) of the expression and activity of the secreted proteins. The anti-(II) antibodies and antagonists may also be used to down regulate expression and activity of (II). The anti-(II) antibodies in samples (e.g. by enzyme linked immunoscrbant assay (ELISA)). The disorders include for example: immune/autoimmune diseases (e.g. HIV (human immunodeficiency virus) infections, anaemia, rheumatoid arthritis and multiple sclerosis), cancers and hyperproliferative disorders (e.g. melanomas, neoplasms of the breast or liver, Sezary syndrome and Gaucher's disease, neurological diseases (e.g. Alzheimer's disease), cancers and hyperproliferative disorders (e.g. cardiac arrest, tachycardia, cardiac arrest, tachycardia, infections caused by bacteria, viruses and fungi and ocular disorders (e.g. cardiac arrest, tachycardia, agonists, antagonists and antibodies can also be used to promote wound conding sequences, PCR primary tissues. AAS33043.AAS33486 represent human secreted protein coding sequences by RCR primers, and related asquences of the invention. Note: The sequence data for this patent did not appear in the printed service in the printed service of primary into the printed service of primary into the printed service of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human secreted protein-encoding gene 11 cDNA clone HCNDV12, SEQ ID NO:21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; secreted protein; proliferative disorder; cancer; tumour; foetal abnormality; haematopoietic disorder; flmnune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; anglogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             17.8%; Score 120; DB 22; Length 804; 100.0%; Pred. No. 5e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Human secreted protein precursor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product "Mature human secreted protein"
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 804 BP; 286 A; 167 C; 208 G; 143 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                      at: ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.08; Pred. ...
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/*tag- a
/product-
193..264
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Matches 120; Conservative
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265..375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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AEA NAD08191-AAD08213 represent CDNAS corresponding to 19 human secreted protein genes, and AAE03764-AAE03786 represent the proteins they encode. C Drotein genes, and AAE03764-AAE03786 represent the proteins they encode. C AAE03787-AAE03800 represent human secreted proteins they encode. C The secreted proteins and their genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene c therapy. Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 19 genes, based on the tissues in which they are most highly expressed, or ordicate disorders, cancer, tumours, foetal and developmental proliferative disorders, cancer, tumours, foetal and developmental aborders, cancer, tumours, foetal and developmental controlling the disorders, diseases of the immune system, altergies, neurological disorders (e.g., rheumatoid arthritis), inflammation, altergies, neurological disorders, disorders, schizophrenia, asthma, cardiovascular disorders, pregnancy-related disorders, and infections. Preparation of subporting call disorders, and infections, preparation, for supporting collustre of primary tissues, to regenerate tissues, to identify their connate ilgands or binding partners, and in chemotaxis, and can be used to sa food additive or preservative to modify storage properties.

C colluter of primary tissues, to regenerate tissues, to identify their connate allowed and allowed as a food additive or preservative to modify storage properties.

Antibodies specific for a protein of the invention can be used an allowance as a food additive or preservative to modify storage properties.

Antibodies specific for a protein of the invention can be used and allowed and allowed contains and allowed and allowed contains and allowed and allowed contains and
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                                                                                                                                                                                          Baker K, Ebner R;
D, Young PE, Florence KA;
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                                                                                                                                                                                                                                                                                                                                 Novel human secreted proteins and nucleic acids for diagnosing, preventing and treating neurological, cardiovascular, infectious, autoimmune, gastrointestinal, bone disorders, cancer, particularly ovarian cancer
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Pred. No. 4.5e-28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1097 BP; 458 A; 182 C; 231 G; 226 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                   L P, Lafleur DW, Olsen HS, Bak
Rosen CA, Ruben SM, Duan RD,
B CE, N1 J, Soppet DR, Sh1 Y;
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100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 380-381; 421pp; English.
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                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC
                                     17-OCT-2000; 2000WO-US28664
                                                                              99US-0163085.
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Best Local Similarity 100.C
Matches 120; Conservative
                                                                                                                                                                                                                               Moore PA, Birse CE,
                                                                                                                                                                                                                                                                  WPI; 2001-328782/34.
P-PSDB; AAE03774.
                                                                                                                                                                                       Wei P,
                                                                              02-NOV-1999;
                                                                                                      17-DEC-1999;
                                                                                                                                                                                     Fiscella M,
                                                                                                                                                                                                         Komatsoulis
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AAD05430
AXB
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AAD05430;

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ADD05389-AAD05473 represent cDNAs corresponding to 29 human secreted protein genes, and AAE01546-AAE01630 represent the protein tragments or variants. AAE016131-AAE0160 represent human secreted proteins tragments or variants. The secreted proteins and their genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the presence of amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the mutations in the new genes. Specific uses are described for each of the mutations in the new genes. Specific uses are described for each of the profile developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, proliferative disorders, diseases of the immune system, allergies, neurological disorders, altahamation, allergies, neurological disorders, schizophrenia, asthma, altanoscaliar disorders, angiogenic disorders, schizophrenia, asthma, shin disorders (e.g., psoriasis), sepsis, diabetes, atheroscalerosis, cardiovascular disorders, pregnancy-related disorders, endocrine disorders, and infections. The proteins can also be used to ald wound challing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their
                                                                                     Human; secreted protein; proliferative disorder; cancer; tumour; foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; sepsis; diabetes; atherosclerosis; cardiovascular disorder; pregnancy-related disorder; pregnancy-related disorder; cell culture; chemotaxis; food additive; gene therapy; binding partner identification; ss.
                                                  Human secreted protein-encoding gene 7 cDNA clone HCNDV12, SEQ ID NO:52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding 29 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease and diabetic retinopathy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'product= "Mature human secreted protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Human secreted protein"
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                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
193..378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 446; 535pp; English
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30-JUN-2000; 2000US-0215137.
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                 17-JUL-2001 (first entry)
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/*tag= b
265..375
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as a food additive or preservative to modify storage properties.
Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic Immunoassays e.g., radioimmunossays or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein-encoding CDNA of the invention.
cognate ligands or binding partners, and in chemotaxis, and can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Central nervous system; CNS; autoimmune disease; rheumatoid arthritis; hyperproliferative disorder; neoplasm; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; ischaemla; angiogenesis; nervous system disorder; Alzheimer's disease; AIDS; ocular disorder; acquired immunodeficiency virus; dysphagia; gastrointestinal disorder; adenocarcinoma; reproductive system disorder; testicular feminisation; endocrine disorder; diabetes; canner; leukaemia; neovascularisation; respiratory disorder; renal disorder; kidney failure; blood disorder; myocardial infarction; wound healing; cell proliferation; skin aging; food additive; food preservative; gene therapy; gene; ss.
                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                  Length 1097;
                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding novel central nervous system protein #76.
                                                                                                                       Sequence 1097 BP; 458 A; 182 C; 231 G; 226 T; 0 other;
                                                                                                                                                                4.5e-28;
                                                                                                                                                  17.8%; Score 120; DB 22;
100.0%; Pred. No. 4.5e-28;
iive 0; Mismatches 0;
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2000US-0225213
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2000US-0184664
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2000US-0198123
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                                                                                                                                                                                     Matches 120; Conservative
                                                                                                                                                      Query Match
Best Local Similarity
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14-AUG-2000;
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14-AUG-2000;
18-AUG-2000;
22-AUG-2000;
22-AUG-2000;
                     22-AUG-2000;
23-AUG-2000;
30-AUG-2000;
01-SEP-2000;
01-SEP-2000;
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(HUMA-) HUMAN GENOME SCI INC 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 01-DEC-2000; 05-DEC-2000; 05-DEC-2000; 05-DEC-2000; 05-JAN-2001; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 08-DEC-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17 - NOV - 2000; 01-DEC-2000; 08-DEC-2000; 08-DEC-2000; 

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-581633/65. P-PSDB; AAU87166.

New isolated nucleic acid encoding a protein for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives -

Claim 1; SEQ ID No 86; 837pp; English.

The invention describes an isolated nucleic acid molecule (I) encoding a novel central nervous system protein. (I) and polypeptides (III) encoded by (I), are used to treat a medical conditions and in diagnosis of a pathological condition. Disorders which are dispassed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, carebrovascular disorders e.g. cardiac arrest, carebrovascular disorders e.g. Alzheimer's disease and amgloderficiency virus (AIDS) and fungi, ocular disorders e.g. dysphagia, e.g. corneal infection, gastrointestinal disorders e.g. dysphagia, adenocarcinomas and irritable bowel syndrome, reproductive system of isorders e.g. testicular feminisation, endocrine disorders e.g. diabetes and pituitary dwarfism, cancers and disorders at the cellular level e.g. leukaemia, disorders involving neovascularisation e.g. malignancies, respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g. acute kidney failure and blood related disorders e.g. myocardial

SSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS	infarction. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein,	Query Match 17.8%; Score 120; DB 23; Length 1194; Best Local Similarity 100.0%; Pred. No. 4.4e-28; Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	557 TCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	617 aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa
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Search completed: June 16, 2003, 06:54:02 Job time : 230.769 secs

Sequence 24, Appl Patent No. 5168051 Sequence 5, Appli Sequence 23, Appl

US-09-372-422A-23 US-08-971-089-5

5168051-9

Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 42, Sequence 42, Sequence 33, Sequence 35, Sequence 35, Sequence 35, Sequence 10, Sequence 11, Sequence 1

US-09-602-877A-95
US-08-811-994-64
US-08-812-994-64
US-08-280-443-1
US-08-55-678-1
PCT-US95-0275-1
US-08-08-658-42
US-09-372-422A-19
US-09-372-422A-19
US-09-372-423-35
US-09-248-335-35
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June 16, 2003, 06:35:31; Search time 47.0496 Seconds (without alignments) 4406.275 Million cell updates/sec
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/cgn2_6/ptodata/1/ina/PcTuS_COMB.seq:*
  GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-443-041A-27
US-09-149-06-11
US-09-104-969-14
US-09-107-369-14
US-09-107-369-1
US-09-071-224-3
US-09-071-224-3
US-09-071-224-3
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US-09-363-708-3
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US-09-297-535-23
                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                         441362 seqs, 153338381 residues
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                        OM nucleic - nucleic search, using sw model
                                                                                                                                                                Post-processing: Listing first 45 summaries
                                                                                       OLIGO_NUC
Gapop 60.0 , Gapext 60.0
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2269
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Match 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17.8%; Score 120; DB 2; Length 20 100.0%; Pred. No. 1.8e-35; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                              MCHUDIA TIETE TELPRY GUERA
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/785,310A
FILING DATE: 21-JAN-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: UTSD:1226
TELEPHONE: (415) 343-4341
TELEPHONE: (415) 343-4341
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                             APPLICANT: MCKAIGHt, Steven L.
APPLICANT: Russell, David W.
TITLE OF INVENTION: Neuronal PAS Domain Protein
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
ALIGNMENTS
                                                                                          Sequence 2, Application US/08785310A Patent No. 5840532 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                        Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 2082 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
                                                                                                                                                                                                                                                                                    CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
2IP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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MOLECULE TYPE: CDNA
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Sequence Sequence Sequence

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APPLICANT: McCOy, John
APPLICANT: LaVallie, Edward
APPLICANT: Racle, Lisa
APPLICANT: Racle, Lisa
APPLICANT: Treacy, David
APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, VIKKI
TILE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: BROODING THEM
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
                                                                                                             Sequence 151, Application US/09370838

Sequence 151, Application US/09370838

GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Secrist, Heather
TILLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
TILLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210.121.475c1
CURRENT APPLICATION NUMBER: US/09/370.838
CURRENT FILING DATE: 1999-08-09
EARLIER PILING DATE: 1999-08-09
SEARLIER PILING DATE: 1999-08-09
SEARLIER FILING DATE: 1999-08-09
SOFTWARE: FILING DATE: 1999-08-05
SOFTWARE: FILING DATE: 1999-08-05
SOFTWARE: FALLS OF UNIDOWS VERSION 3.0
SOFTWARE: FALLS OF UNIDOWS VERSION 3.0
SEQ ID NO 151
LENGTH: 3275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 3275;
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PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 17.6%; Score 119; DB 4; I Best Local Similarity 100.0%; Pred; No. 3.8e-35; Matches 119; Conservative 0; Mismatches 0;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Jacobs, Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02140
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                                                                                                     US-09-370-838-151
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Gaps

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17.5%; Score 118; DB 1; Length 240; 100.0%; Pred. No. 1.5e-34;
                                                                                                                                                                                                                                                                                 Length 144;
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SOFTWARE: PATCHTIN RELease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/628,417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: GILLESPIE, DAVID
TITLE OF INVENTION: COMPETITOR PRIMER ASYMMETRIC
TITLE OF INVENTION: POLYMERASE CHAIN REACTION
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: U.S. ARMY CHEMICAL AND BIOLOGICAL ADDRESSEE: DEFENSE COMMAND STREET: OFFICE OF THE CHIEF COUNSEL (AMSCB-GC) CITY: ABREDEEN PROVING GROUND STATE: MARYLAND
                                                                                                                                                                                                                                                                                     17.5%; Score 118; DB 1; 100.0%; Pred. No. 1.7e-34;
                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: BIFFONI, ULYSSES J
REGISTRATION NUMBER: 39,908
REFERNCE/DOCKET NUMBER: DAM 398-94
TELECOMMUNICATION INFORMATION:
TELEPHONE: 410-671-1158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: oligodeoxynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/08628417
Patent No. 5627054
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS_
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,72,
TELECOMMUNICATION INFORMATION
TELEPHONE: (617) 498-8224
                                                          TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEO ID NO: 26
SEQUENCE CHARACTERISTICS:
                                                                                                                                          ; LENGTH: 144 base pairs; TYPE: nucleic acid; STRANDEDNESS: double; TOPOLOGY: linear; MOLECULE TYPE: cDNAUS-08-702-344-26
                                                                                                                                                                                                                                                                                         Query Match 17.5
Best Local Similarity 100.
Matches 118; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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APPLICANT: Zianghe YAN, Karen A. KETCHUM, Valentina DIFRANCESCO, Ellen M. BEASLEY TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS, TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND TITLE OF INVENTION: USES THEREOF PLLE REFERENCE: CLOOLISICIP CURRENT APPLICATION NUMBER: US/09/797,906
CURRENT PAPLICATION NUMBER: US/09/797,906
CURRENT FILING DATE: 2011-03-05
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1.
                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
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APPLICANT: Racie, Lisa A.
APPLICANT: Merberg, David
APPLICANT: Tracay, Maurice
APPLICANT: Spaulding, Vikki
APPLICANT: Agostino, Michael J.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: BROODING THEM
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17.5%; Score 118; DB 4;
100.0%; Pred. No. 9.9e-35;
iive 0; Mismatches 0;
                          Mismatches
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87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 14, Application US/09014969
Patent No. 5965397
                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09797906
Patent No. 6329188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jacobs, Kenneth
McCoy, John M.
LaVallie, Edward R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.(
Matches 118; Conservative
                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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APPLICANT: Jacobs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 87 Cambraction CITY: Cambraction
                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Human
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                    Matches 118;
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                                                                                                                                                                                                                                                                                                                      US-09-797-906-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND TREATMENT TITLE OF INVENTION: OF BODY WEIGHT DISORDERS INCLUDING OBESITY FILE REFERENCE: 7853-136
CURRENT APPLICATION NUMBER: US/09/245,041
CURRENT FILING DATE: 1999-02-05
EARLIER FILING DATE: 1999-07-21
EARLIER FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 131
SOFTWARE: FASLERG for Windows Version 3.0
EENGTH: 1051
                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1447;
               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 27, Application US/09443041A
Fatent No. 6465717
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Famedu, Omolayo O.
APPLICANT: Rafalski, Antoni
APPLICANT: Rafalski, Antoni
APPLICANT: Rafalski, Antoni
APPLICANT: Shen, Jennel
TILLE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/443,041A
PRIOR APPLICATION NUMBER: 60/109,283
PRIOR APPLICATION NUMBER: 60/109,283
SOFTWARE: Microsoft Office 97
LENGTON NO 27
LENGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 118; DB 4;
Pred. No. 1e-34;
       0; Mismatches
                                                                                                                                                                                                                                                                                                    US-09-245-041-10

Sequence 10, Application US/09245041;

Patent No. 6274339

GENERAL INFORMATION:
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100.0%;
Matches 118; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Mus musculus US-09-245-041-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Glycine max
.US-09-443-041A-27
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Moore, K. APPLICANT: Nagle, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Simi
Matches 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -09-443-041A-27
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Length 117;
                  APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
TITLE OF INVENTION: ENCODING THEM
TITLE OF INVENTION: ENCODING THEM
                                                                                                                                                                                                                              COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TIBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702,344
FILING DATE:
CLASSIFICATION S36
ATTORNEY/AGENT INFORMATION:
NAME: BEOWN, Scott A.
REGISTRATION NUMBER: 32,724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 17.3%; Score 117; DB 1; Best Local Similarity 100.0%; Pred. No. 4.1e-34; Matches 117; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: DOS
SOFTWARE: FastEGO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Grossmann, Angelika
TITLE OF INVENTION: NOVEL TUMOR ANTIGENS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: TymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
                                                                                               NUMBER OF SEQUENCES: 37
CORRESSPONDENCE ADDRESS:
STREET: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09073569 Patent No. 6084088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-824
TELEPAX: (617) 876-5821
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
Merberg, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 117 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                            CITY: Cambridge
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM COM OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                      COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-702-344-3
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Patent No. 6340584
GENERAL INFORMATION:
FOR A PAPLICANT: COMPATION:
FITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
FILE REPERBNCE: CLO01183
CURRENT FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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17.5%; Score 118; DB 4; Length 2674;
Best Local Similarity 100.0%; Pred. No. 9.1e-35;
Matches 118; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                Length 2447;
                                                                                                                                                                                                                                                                                                                                                           Query Match
17.5%; Score 118; DB 2; I
Best Local Similarity 100.0%; Pred. No. 9.3e-35;
Matches 118; Conservative 0; Mismatches 0;
        APPLICATION NUMBER: US/09/014,969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/08702344; Patent No. 5723315
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: MCCOY, John
APPLICANT: LaVallie, Edward
APPLICANT: Racie, Lisa
                                                            ATTORNEY AGENT INFORMATION:
NAME: Sprunger, Suzanne A.
REGISTRATION NUMBER: 41,323
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8284
TELEPAX: (617) 498-8284
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                            LENGTH: 2447 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-09-014-969-14
                               FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
CRGANISM: Human
US-09-817-180-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 1
LENGTH: 2674
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US-08-702-344-3
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Sequence 1, Application US/09394645
Patent No. 6380371
               REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEPAX: 206-442-6678
                                                                                                                                                                                                                            NAME/KEY: Coding Sequence LOCATION: 88...1362
CTHER INFORMATION:
US-09-071-224 -3
                                                                                           INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 1813 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.C
Matches 114; Conservative
                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
REGISTRATION NUMBER:
                                                                                                                                                                   TOPOLOGY: 11near
MOLECULE TYPE: CDNA
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: human
US-09-394-645-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-243-560B-1
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US-09-394-645-1
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                                                                                                                                                                                                                                                                                                                                                                                                             Length 1733;
                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                      17.3%; Score 117; DB 3; I 100.0%; Pred. No. 2.3e-34; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lok, SI
APPLICANT: Dresnell, Scott R.
APPLICANT: Jeluberg, Anna C.
APPLICANT: Gllbert, Teresa
APPLICANT: Goster, Donald C.
APPLICANT: Adams, Robyn L.
APPLICANT: Lehner, Joyce M.
TITLE OF INVENTION: MAMMALIAN ZCYTORS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Zymogenetics
1201 Eastlake Ave East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/09071224 Patent No. 6271343 GENERAL INFORMATION:
                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A
REGISFRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 97-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
                                                                                                                                                                                                                                                                                                                       ) NAME/KEY: Coding Sequence

) LOCATION: 34...1344

) OTHER INFORMATION:

US-09-073-569-1
                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 1733 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 17.3' Best Local Similarity 100. Matches 117; Conservative
                                                                                                                                                                      TELEFAX: 206-442-6678
     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                          linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seattle
                                                                                                                                                                                                                                                                     STRANDEDNESS:
TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-071-224-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING
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APPLICANT: Sassetti, Christopher M.
APPLICANT: Sassetti, Christopher M.
APPLICANT: Rosen, Steven R.
TILLE OF INVENTION: Endoglycan: A NOVEL PROTEIN HAVING SELECTIN
TILLE OF INVENTION: LIGAND AND CHEMOKINE PRESENTATION ACTIVITY
FILE REFERENCE: 6510-122US1
CURRENT APPLICATION NUMBER: US/09/394,645
CURRENT FILING DATE: 1999-09-13
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 3.0
      Length 1813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 2269;
                                           Indels
Query Match 17.2%; Score 116; DB 4; I
Best Local Similarity 100.0%; Pred. No. 5.2e-34;
Matches 116; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09243560B
Patent No. 6395882
GENERAL INFORMATION:
APPLICANT: Sassetti, Christopher M.
APPLICANT: Sassetti, Christopher M.
TITLE OF INVENTION: No. 6395882el Selectin Ligands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 2.6e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16.9%; Score 114; DB 4;
100.0%; Pred. No. 2.6e-33
Live 0; Mismatches 0
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                                                                                                                                                                                                                                                                     Length 2269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/363,708
                                                                                                                                                                                                                                                                        Query Match 16.9%; Score 114; DB 4; Best Local Similarity 100.0%; Pred. No. 2.6e-33; Matches 114; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 16.7%; Score 113; DB 4; Best Local Similarity 100.0%; Pred. No. 6.1e-33; Matches 113; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Schmandt, et al.
TITLE OF INVENTION: NOVEL SHC BINDING PROTEIN
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/34451
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEPHONE: (312) 474-6300
TELEPAN: (312) 474-6448
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
FILE REFERENCE: UCAL097US1
CURRENT APPLICATION NUMBER: US/09/243,560B
CURRENT FILING DATE: 1999-02-03
PRIOR APPLICATION NUMBER: US 60/074,389
PRIOR FILING DATE: 1998-02-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , MOLECULE TYPE: CDNA;
; DESCRIPTION: /desc = "mouse PAL cDNA"
US-09-363-708-3
                                                                                                    NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
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Patent No. 6399747
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CORGANISM: Homo sapiens
US-09-243-560B-1
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STRANDEDNESS: sing
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STATE: Illino:
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Search completed: June 16, 2003, 08:47:01 Job time: 54.0496 secs

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GenCore version 5.1.6

Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 16, 2003, 07:57:31; Search time 149.802 Seconds

(without alignments)
6534.570 Million cell updates/sec

Title: US-10-090-035-1

Sequence: 1 acccacgcgtccgccacgc.....aaaaaaaaaaaaa 676

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 1029858 seqs, 724030393 residues

Word size: 0

Total number of hits satisfying chosen parameters: 2059716

Minimum DB seq length: 200000000

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries
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Published\_Applications\_NA:\*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		ìn		Sequence 3, Appl1	Sequence 0 Appli		, , ,	Ç		Sequence 21, Appr	Sequence 38, Appl	Seguence 106, App	ú			Seduence /491, Ap	Sednence 9815, Ap	Sequence 344, App	Sequence 1301, Ap	•
SOMMAKIES	ΙD	US-10-090-035-1	US-10-090-035-3	US-10-090-035-5	US-10-090-035-7	US-10-090-035-9	US-10-090-035-17	US-10-125-540-76	US-09-764-870-76	US-09-832-129-21	8E-028-876-50	US-10-239-676-106	US-09-960-352-11058	US-09-764-872-709	US-10-061-483	US-09-764-891-7491	16+/ 160 +0/ 60 GD	CT06-T60-%0/-60 CO	03-03-704-840-344	US-09-960-352-1301	US-09-960-352-6539
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	Score	929	313	313	261	188	169	121	121	120	120	120	119	119	119	119	119	119	1.	113	113
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Sequence 37, Appl Sequence 4765, Appl Sequence 465, Appl Sequence 465, Appl Sequence 465, Appl Sequence 465, Appl Sequence 21, Appl Sequence 21, Appl Sequence 212, Appl Sequence 27, Appl	Inducible	100.0%; Score 676; DB 9; Length 676; ; Conservative 0; Mismatches 0; Indels 0; Gaps 0; ACCCAGGGTCGGCCCAGGGATCCACACAGAGCACTTGAAGGACCACTGG 60
US-09-822-849A-37 US-09-878-574-4765 US-10-012-542-44 US-10-076-622-465 US-09-551-621-465 US-09-551-621-465 US-09-551-621-465 US-09-64-287A-465 US-09-007-805-465 US-09-729-674-67 US-09-729-674-67 US-09-907-81212 US-09-907-81212 US-09-907-81212 US-09-907-81212 US-09-907-81212 US-09-907-81212 US-09-907-81212 US-09-907-81212 US-09-907-81212 US-09-907-81212 US-09-907-81212 US-09-907-81212 US-09-907-81212 US-09-907-81212 US-09-907-81212 US-09-907-81212 US-09-907-81212 US-10-176-758-27 US-10-176-758-27 US-10-176-782-27 US-10-176-782-27 US-10-176-782-27 US-10-176-782-27 US-10-176-782-27	ALIGR Encc Uses 7090, 227	Score 676; DB 9; Pred. No. 0; 0; Mismatches 0; CGTCCGCAGCAATCCACAL
409 495 574 674 674 674 10 674 10 674 10 674 10 683 10 10 10 10 10 10 10 10 10 10	n US/10 89A1 arl R. ucleic Vorcein 7242990 WmBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0MBER: 0	larity 100.0%; Conservative ( CACGCGTCCGCCCACG( 
177.6 177.6 177.6 177.6 177.6 177.6 177.6 177.6 177.6 177.6 177.6 177.6 177.6	5-1  Vaplicatio US20201170 US20201170 US20201170 USAUMONS CONATION: NINVENTION: RENCE: 35718 PPDICATION NUM ULING DATE: LICATION NUM UNG DATE: LICATION NUM CONTROL OF CONTROL O	Similarity 6; Conser ACCCACGCG                     ACCCACGCG
1119 1119 1119 1119 1119 1119 1119 111	SGULT 1 Sequence 1, Applicat Beatent No. US202017 BENEAL INFORMATION: TITLE OF INVERTIONS, TITLE OF INVERTION: FILE REFERENCE: 357 CURRENT APPLICATION CURRENT APPLICATION CURRENT FILING DATE: PRIOR FILING DATE: PRIOR PILING DATE: NUMBER OF SEQ ID NO SOFTWARE: FastSEQ f SEQ ID NO SOFTWARE: PASTSEQ f TYPE: DNA CORGANISM: Zea mays FEATURE: NAME/KEY: CDS LOCATION: (89)(CATION: (40)(CATION: (40)(CATION: (40)(CATION: (40)(CATION: (40)(CATION: (40)(CATION: (40)(CATION: (40)(CATION: (40)(CATION: (40	h 76 1
0 000000000000000000000000000000000000	RESULT 1 US-10-090-0 Sequence Patent NO GENERAL I TITLE OF ORGANIS TYPE: DI ORGANIS FEATURE CRATURE INMEKEN CRATURE INMEKEN	Query Matc Best Local Matches 6 Qy Db

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CCGGCATCCACGCCCGTTCGTGCTTGCCTGCGTATGTTATGTCTGTGGTTGACTGG 442
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                      GGCGAGGTCCACGAGGCAGGGAGGCTTCCTCGCCAGGGCTAACTGAGCCGCCGGCGG
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APPLICATE: Simmons, Carl R.

TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible SITLE OF INVENTION: Proteins and Uses Thereof CURRENT APPLICATION NUMBER: US/10/090,035

CURRENT FILING DATE: 2002-02-28

PRIOR APPLICATION NUMBER: 60/272,227

NUMBER OF SO ID NOS: 25
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Pred. No. 9.9e-144;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/10090035 Patent No. US20020170089A1 GENERAL INFORMATION:
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ilarity 99.4%;
Conservative
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US-10-090-035-5
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Best Local Similarity
Matches 463; Conserv
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LENGIH: 577
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US-10-090-035-5
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Sequence 3, Application US/10090035
Patent No. US20020110089A1
GENERAL INFORMATION:
APPLICANT: SIMMONS, CAIT R.
TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible
TITLE OF INVENTION: Proteins and Uses Thereof
FILE REFERENCE: 35718/742990
CURRENT APPLICATION UNBER: US/10/090,035
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 60/272,227
PRIOR FILING DATE: 02/28/2001
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Pred. No. 9.9e-144;
0; Mismatches 3; Indels
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SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 99.4%;
Matches 463; Conservative
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US-10-090-035-3
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ORGANISM: Zea mays
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US-10-090-035-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: SIGNATION: Carl R.
TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible
TITLE OF INVENTION: Proteins and Uses Thereof
FILE REFERENCE: 35718/242990
CURRENT APPLICATION NUMBER: US/10/090,035
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 60/272,227
PRIOR APPLICATION NUMBER: 60/272,227
PRIOR RILING DATE: 02/284/2001
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 524;
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Best Local Similarity 100.0%; Pred. No. 3.5e-73;
Matches 169; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                               Score 188; DB 9;
Pred. No. 1.7e-82;
0; Mismatches 2
CURRENT APPLICATION NUMBER: US/10/090,035
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 60/272,227
PRIOR FILING DATE: 02/28/2001
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PastSEQ for Windows Version 4.0
LENGTH: 529
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99.3%;
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ORGANISM: Triticum aestivum
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Best Local Similarity 99.39
Matches 288; Conservative
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LOCATION: (1)...(524)
OTHER:INFORMATION: n =
                                                                                                                                                                                                                   ; NAME/KEY: CDS
; LOCATION: (53)...(331)
US-10-090-035-9
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LOCATION: (57)...(338)
                                                                                                                                                                            ORGANISM: Zea mays
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                                                                                                                                                           TYPE: DNA
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                                                               297 TCGAGGAGGACATCAACACCTGCACCGGCGAGGTCCACGAGCGCAGGGAGGCTTCCTCG 356
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  443 TIGIGCAGGGTCATCGTACTIGGCTATCGTACGTGCACGCACTCAGCTCCTGTACGAATT 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        237 ACCACCACCACCATGGTCACCACGGCGGCCACGGCTTCGTGGTGCGCGAGACCAGGG
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                                                                                                                                                                                                                                                    Sequence 7, Application US/10090035
Patent No. US20020170089A1
GENERAL INFORMATION:
TILL INFORMATION:
TITLE OF INVENTION: Nucleic Acids Encoding Defense Inducible
FILE REFERENCE: 35718/244990
CURRENT APPLICATION NUMBER: US/10/090,035
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 60/272,227
PRIOR FILING DATE: 02/28/2001
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                  503 ACGACAATAAGCTCGTGACCTGAATAAAACTTCTTCGTAATACTAA 548
                                                                                                                                       Sequence 9, Application US/10090035
Patent No. US20020170089A1
GENERAL INFORMATION:
APPLICANT: Simmons, Carl R.
TITLE OF INVENTION: NUCLEIC Acids Encoding Defense Inducible
TITLE OF INVENTION: Proteins and Uses Thereof
FILE REFERENCE: 35718/242990
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Pred. No. 2.9e-118;
0; Mismatches 1;
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Best Local Similarity 99.7%;
Matches 311; Conservative
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; LOCATION: (99)...(380)
US-10-090-035-7
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Best Local Similarity
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US-09-948-820-38
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                  919
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                                                                                                           357 CCAGGGCTAACTGAGCCGCCCGGCGCCGGCATCCACGCCCGTTCGTGC 405
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT14
CURRENT FILING DATE: 2001-01-17
FIG. Application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 646
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 76
LENGTH: 2645
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                                                                                                                                                                                           Sequence 75, Application US/10125540
Publication No. US20030059875A1
GENERAL INFORMATION:
TILLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PT214C1
CURRENT APPLICATION NUMBER: US/10/125,540
CURRENT FILING DATE: 2002-04-19
PILOT APPLICATION NUMBER: 05.002-04-19
SIGHT APPLICATION NUMBER: 05.002-04-19
PILOT APPLICATION NUMBER: 2002-04-19
SOFTWARE: PATENTIN VET. 2.0
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Best Local Similarity 100.0%; Pred. No., 9.6e-50;
Matches 121; Conservative 0; Mismatches 0;
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Pred. No. 9.6e-50;
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Matches 121; Conservative
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; ORGANISM: Homo sapiens
US-10-125-540-76
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US-09-764-870-76
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                                                                                                                                                                                                                                                                APPLICANT: Fiscella et al.
TITLE OF INVENTION: 19 Human secreted proteins
FILE REFERENCE: P2045P1
CURRENT APPLICATION NUMBER: US/09/832,129
CURRENT FILING DATE: 2001-04-11
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 1999-11-02
PRIOR FILING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PATENTING DATE: 1999-12-17
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Publication No. US20030050460A1
GENERAL INFORMATION:
APPLICANT: Ni et al
IITLE OF INVENTION: 31 Human Secreted Proteins
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CURRENT APPLICATION NUMBER: US/09/948,820
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: US/09/565,391
PRIOR PILING DATE: 2000-05-05
PRIOR PELICATION NUMBER: PCT/US99/26409
PRIOR PELICATION NUMBER: 60/108,207
PRIOR APPLICATION NUMBER: 60/108,207
PRIOR FILING DATE: 1999-11-12
                                                                                                                                                                                          Sequence 21, Application US/09832129
Publication No. US20030027297A1
GENERAL INFORMATION:
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Matches 120; Conservative
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SEQ ID NO 38
LENGTH: 1457
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US-09-832-129-21
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US-09-948-820-38
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ORGANISM: Homo sapiens
US-09-764-872-709
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US-10-091-483-344
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Patent No. US20020137139A1
GENERAL INCOMPATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
                                                                                                                                                                                                                                                                   APPLICANT: OLEK, Alexander
APPLICANT: PEPENBROCK, Christian
APPLICANT: BEREIN, Kurt
TTYLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation
FILE REFERENCE: 5013.1003
CURRENT PAPLICATION NUMBER: US/10/239,676
CURRENT PILING DATE: 2002-09:24
PRIOR APPLICATION NUMBER: PCT/EP01/03968
DE 10019058.8
DE 10019058.8
DE 10032529.7
DE 10043826.1
PRIOR FILING DATE: 2001-04-06
2000-04-06
2000-04-06
2000-06-30
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LOCATION: (2778, 2845..2846, 2865, 2916, 9325, 10589, 10612, 10809, 10817)
       Gaps
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; LOCATION: (10821, 10827, 10830..10831, 10839, 12552, 13433, 15042)
US-10-239-676-106
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17.8%; Score 120; DB 9; I
Best Local Similarity 100.0%; Pred. No. 2.5e-49;
Matches 120; Conservative 0; Mismatches 0;
   Mismatches
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Publication No. US20030082609A1
GENERAL INFORMATION:
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Matches 120; Conservative
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NUMBER OF SEQ ID NOS: 228
SEQ ID NO 106
LENGTH: 15832
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                                                                                                                                                                                                                                       Length 160;
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CURRENT APPLICATION NUMBER: US/09/764,872
CURRENT FILING DATE: 2001-01-17
PLIOT APPLICATION data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 957
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT21.2C1
CURRENT APPLICATION NUMBER: US/10/091,483
CURRENT FILING DATE: 2002-03-07
CURRENT FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 348
Prior Application removed - See File Wrapper or Palm
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 344
LENGTH: 165
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                                                                                                                  ; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 47-LIB34-055-Q1-E1-D12
US-09-960-352-11058
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CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 11058
LENGTH: 160
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Publication No. US20030049650A1
GENERAL INFORMATION:
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Sequence 7491, Application US/09764891
Publication No. US2003007780841
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TILLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 10231
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7491
LENGTH: 165
Length 165;
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Best Local Similarity 100.0%; Pred. No. 1.2e-48;
Matches 119; Conservative 0; Mismatches 0;
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CORGANISM: Homo sapiens
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Search completed: June 16, 2003, 10:24:24 Job time : 155.802 secs

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BASE COUNT ORIGIN

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BQ619318 648 bp mRNA linear EST 27-JUN-2002 RNOSEQ6D01_SK.abl Salt stressed Zea mays roots CDNA library Zea mays CDNA clone RNOSEQ6D01_SK.abl similar to No homology, mRNA
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                                                           Location/Qualifiers

1. 648

/organism=2ea mays*
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/tlosue_lib="Salt stressed Zea mays roots cDNA library*
/tlosue_lib="Roots"
/tlosue_type="Roots"
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mM Nacl"
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Pred. No. 1.5e-46;
0; Mismatches 14; Indels
          University of Illinois
1201 W. Gregory Dr., Urbana, IL 61801, USA
Tel: 2172655473
Email: bohnertlab@life.uiuc.edu.
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Eukaryota, Magnoliophyta; Liliopsida; Poales; Toaceae; PACC
clade; Panicodidaee; Andropogoneae; Zea.
1 (bases 1 to 648)
Mangi,H. and Bohnert,H.J.
Genomits of plant stress tolerance
Unpublished (2002)
                                              at 150
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      mays roots cDNA library'
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Pred. No. 1.5e-46;
0; Mismatches 14; Indels
/clone_lib="Salt stressed Zea ma
/tissue_type="Roots"
/dev_stage="2 weeks old"
/note="Vector: pBluescript SK+;
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Department of Plant Biology
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ilarity 96.98;
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clade, Panicoldeae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                         /organism="Zea mays"
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/clone="In="Sait stressed Zea mays roots cDNA library"
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/dev_stage="2 weeks old"
/note="Vector: pBluescript SK+; Stressed 24 hours at 150
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cuxaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

"I (bases 1 to 648)
"ORS Wang H. and Bohnert.H.J.
E Genomics of plant stress tolerance
"NAL Unpublished (2002)
"Contact: Mark Fredricksen
Departument of Plant Billogy
University of Illinois
"I2101 W. Gregory Dr., Urbana, IL 61801, USA
Tel: 2172655473
Email: bohnertlab@life.uluc.edu.
"Locatlon/Qualiflers
rce 1..648
BQ619337 648 bp mRNA linear EST 27-JUN-2002 RNOSEQGE12_SK.abl Salt stressed Zea mays roots cDNA library Zea mays cDNA clone RNOSEQ6E12_SK.abl similar to No homology, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Zea mays"
/db_xref="taxon:4577"
/clone="RNOSEQ6E12_SR.ab1"
/clone_llb="Salt stressed Zea mays roots cDNA library"
/tissue_type="Roots"
/dev_stage="2 weeks old"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGTCAAGGAGAAGTTCGAGGAGGTCGACACGGTATCACGCGCCGGCGCCCA---ACCACCA
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Pred. No. 1.5e-46;
0; Mismatches 14
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